

Result No.	Score			Match	Length	DB	ID	Description
	Score	Match	Length					
1	327	100.0	482	4	US-09-513-999C-3894	Sequence 3894, Ap		
2	327	100.0	507	4	US-09-949-016-4940	Sequence 4940, Ap		
3	253.6	77.6	3208	4	US-09-780-016-27	Sequence 27, Appl		
4	253.6	77.6	3208	4	US-10-214-811-27	Sequence 27, Appl		
5	170	52.0	402	4	US-09-513-999C-10371	Sequence 10371, A		
6	170	52.0	463	4	US-09-621-976-15180	Sequence 15180, A		
7	153.2	46.9	411	4	US-09-640-211A-1731	Sequence 1731, Ap		
8	138.2	42.3	490	4	US-09-270-767-26812	Sequence 26812, A		
9	138.2	42.3	1101	4	US-09-270-767-11265	Sequence 11265, A		
10	114.4	35.0	357	4	US-09-248-736A-5495	Sequence 5495, Ap		
11	92.6	28.3	25274	4	US-09-949-016-16682	Sequence 16682, A		
12	90	27.5	301	4	US-09-313-294A-492	Sequence 492, App		
13	74	22.6	342	4	US-09-826-312A-7	Sequence 7, Appli		
14	74	22.6	342	4	US-09-542-497A-7	Sequence 7, Appli		
15	46.4	14.2	439	4	US-09-799-451-296	Sequence 296, App		
16	36	11.0	601	4	US-09-949-016-174803	Sequence 174803, A		
17	33.6	10.3	87734	4	US-09-949-016-17521	Sequence 17521, A		
18	33.4	10.2	170	4	US-09-270-767-26253	Sequence 26253, A		
19	33.4	10.2	585	4	US-09-270-767-10788	Sequence 10788, A		
20	33	10.1	601	4	US-09-949-016-120325	Sequence 120325, A		
21	33	10.1	219964	4	US-09-949-016-15086	Sequence 15086, A		
22	32.6	10.0	96845	4	US-09-949-016-13658	Sequence 13658, A		
23	31	9.5	2408	1	US-08-608-241-1	Sequence 1, Appli		
24	31	9.5	2408	2	US-08-922-182-1	Sequence 1, Appli		
25	31	9.5	2408	2	US-08-919-953-1	Sequence 1, Appli		
26	31	9.5	2408	3	US-09-192-983-1	Sequence 1, Appli		
27	30.4	9.3	119762	4	US-09-949-016-17313	Sequence 17313, A		

QY 181 GCGTCGCTACTTTCAGAGAGTGTACTGTCGATGGGGAGTCTGTAAACCATGCTTTTCAC 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
209 GCGTCGCTACTTTCAGAGAGTGTACTGTCGATGGGGAGTCTGTAAACCATGCTTTTCAC 268
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGCCATTGGACCAACAGAGAG 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
269 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGCCATTGGACCAACAGAGAG 328
QY 301 TGGGAATTCCAAAGTATGGCACTAG 327
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
329 TGGGAATTCCAAAGTATGGCACTAG 355

RESULT 2
US-09-949-016-4940
; Sequence 4940, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4940
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4940

Query Match 100.0%; Score 327; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 1.9e-107; Indels 0; Gaps 0;
Matches 327; Conservative 0; Mismatches 0

QY 1 ATGCGCGCAGCGATGGATGGATACCCGAGCGGACCAACAGCGCGCGGSCAAGAAG 60
Db 7 ATGCGCGCAGCGATGGATACCCGAGCGGACCAACAGCGCGCGGSCAAGAAG 66

QY 61 CGCTTTGAAGTGAAGTGAATGCAATGAGTATGATGATGATGATGATGATGATGAT 120
Db 67 CGCTTTGAAGTGAAGTGAATGCAATGAGTATGATGATGATGATGATGATGATGAT 126

QY 121 AACTGTGCCATCTGCGAGGACCAACATATGATGATGATGATGATGATGATGATGAT 180
Db 127 AACTGTGCCATCTGCGAGGACCAACATATGATGATGATGATGATGATGATGATGAT 186

QY 181 GCGTCGCTACTTTCAGAGAGTGTACTGTCGATGGGGAGTCTGTAAACCATGCTTTTCAC 240
Db 187 GCGTCGCTACTTTCAGAGAGTGTACTGTCGATGGGGAGTCTGTAAACCATGCTTTTCAC 246

QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGCCATTGGACCAACAGAGAG 300
Db 247 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGCCATTGGACCAACAGAGAG 306

QY 301 TGGGAATTCCAAAGTATGGCACTAG 327
Db 307 TGGGAATTCCAAAGTATGGCACTAG 333

RESULT 3
US-09-780-016-27
; Sequence 27, Application US/09780016
; Patent No. 6509456
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory

; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/09/780, 016
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-780-016-27

Query Match 77.6%; Score 253.6; DB 4; Length 3208;
Best Local Similarity 98.5%; Pred. No. 1.7e-80; Indels 0; Gaps 0;
Matches 256; Conservative 0; Mismatches 4

QY 68 AAGTGAAGTGAATGCAATGAGTATGATGATGATGATGATGATGATGATGATGATG 127
Db 2765 AAAAAAAAAATGGAATGCAATGAGTATGATGATGATGATGATGATGATGATGATG 2824

QY 128 CCATCTGCAGGAACCAACATATGATGATGATGATGATGATGATGATGATGATGATG 187
Db 2825 CCATCTGCAGGAACCAACATATGATGATGATGATGATGATGATGATGATGATGATG 2884

QY 188 CTACTTCAGAGAGTGTACTGTCGATGGGGAGTCTGTAAACCATGCTTTTCACCT 247
Db 2885 CTACTTCAGAGAGTGTACTGTCGATGGGGAGTCTGTAAACCATGCTTTTCACCT 2944

QY 248 GCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATGGAATGTCGATGGAAT 307
Db 2945 GCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCATGGAATGTCGATGGAAT 3004

QY 308 TCCAAAAGTATGGCACTAG 327
Db 3005 TCCAAAAGTATGGCACTAG 3024

RESULT 4
US-10-214-811-27
; Sequence 27, Application US/10214811
; Patent No. 6743621
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/10/214,811
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/780,016
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,294
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens

US-10-214-811-27

Query Match 77.6%; Score 253.6; DB 4; Length 3208;
Best Local Similarity 98.5%; Pred. No. 1.7e-80;
Matches 256; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 68 AAGTGAAGAGTGGATGAGTACAGTACGCTCGGCTGGGATATGTTGATTAACCTGTG 127
Db 2765 AAAAAAAAAATGGAATGCAATGAGTACGCTCGGCTGGGATATGTTGATTAACCTGTG 2824
Qy 128 CCATCTGCAGGAACACATTAATGATCTTTGATAGAATGTCAAGCTAACCCAGGCGTCCG 187
Db 2825 CCATCTGCAGGACACATTAATGATCTTTGATAGAATGTCAAGCTAACCCAGGCGTCCG 2884
Qy 188 CTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACATGCTTTTCACTTCCACT 247
Db 2885 CTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACATGCTTTTCACTTCCACT 2944
Qy 248 GCATCTCTCGCTGCTCAAAACACGACAGGTGTGTCATTTGGACAACAGAGTGGGAAT 307
Db 2945 GCATCTCTCGCTGCTCAAAACACGACAGGTGTGTCATTTGGACAACAGAGTGGGAAT 3004
Qy 308 TCCAAAAGTATGGGCACTAG 327
Db 3005 TCCAAAAGTATGGGCACTAG 3024

RESULT 5

US-09-513-999C-10371
; Sequence 10371, Application US/09513999C
; Patent No. 6783961

; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10371
; LENGTH: 402

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 20
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 38
; OTHER INFORMATION: s=g or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 79
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-10371

Query Match 52.0%; Score 170; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 7.2e-51;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 GCATAGAATGTCAGCTAACCGGGCTCGCTACTTTCAGAGAGTGTACTGTGCGATCGG 217
Db 106 GCATAGAATGTCAGCTAACCGGGCTCGCTACTTTCAGAGAGTGTACTGTGCGATCGG 165
Qy 218 GAGTCTGTAAACATGCTTTTCACTTCCACTGCTCTCGCTGGCTCAAAACACGACAGG 277
Db 166 GAGTCTGTAAACATGCTTTTCACTTCCACTGCTCTCGCTGGCTCAAAACACGACAGG 225

Qy 278 TGTGTCCATTGGACAACAGAGAGTGGGAATTCCTCAAAAGTATGGGCACTAG 327
Db 226 TGTGTCCATTGGACAACAGAGAGTGGGAATTCCTCAAAAGTATGGGCACTAG 275

RESULT 6

US-09-621-976-15180
; Sequence 15180, Application US/09621976
; Patent No. 6639063

; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15180
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 74
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-15180

Query Match 52.0%; Score 170; DB 4; Length 463;
Best Local Similarity 100.0%; Pred. No. 7.9e-51;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 158 GCATAGAATGTCAGCTAACCGGGCTCGCTACTTTCAGAGAGTGTACTGTGCGATCGG 217
Db 101 GCATAGAATGTCAGCTAACCGGGCTCGCTACTTTCAGAGAGTGTACTGTGCGATCGG 160
Qy 218 GAGTCTGTAAACATGCTTTTCACTTCCACTGCTCTCGCTGGCTCAAAACACGACAGG 277
Db 161 GAGTCTGTAAACATGCTTTTCACTTCCACTGCTCTCGCTGGCTCAAAACACGACAGG 220

Qy 278 TGTGTCCATTGGACAACAGAGAGTGGGAATTCCTCAAAAGTATGGGCACTAG 327
Db 221 TGTGTCCATTGGACAACAGAGAGTGGGAATTCCTCAAAAGTATGGGCACTAG 270

RESULT 7

US-09-640-211A-1731

; Sequence 1731, Application US/09640211A
; Patent No. 6833446

; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021C1U
; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1731
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Pinus radiata
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(411)
; OTHER INFORMATION: n = A, T, C or G
US-09-640-211A-1731

Db	269	ATTTCATTTGTTATTAAGATGTTTGAACAAGAAATGCATGTCCCTTGGATAGTACTA	328
Qy	299	AGTGGGAATTCCAAAAGTATGGGCACTA	326
Db	329	ATTGGACTTATCAAAAATTTGGGTAATTA	356

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RESULT 11
US-09-949-016-16682
; Sequence 16682, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16682
; LENGTH: 25274
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16682

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	Query Match	28.3%	Score 92.6	DB 4	Length 25274
	Best Local Similarity	96.0%	Pred. No. 6.7e-22		
	Matches 9	Conservative 0	Mismatches 4	Indels 0	Gaps 0
Qy	221	TCGTGAACCAAGCTTTTTCACATCTCCATCGCATCTCGCTGGGTCAAAACACACACAGGTGT	280		
Db	18403	TCYTTGAGCAATGCTTTTTCATCTCCATCGCATCTCGCTGGGTCAAAACACACACAGGTGT			
Qy	281	GTCCATTGGACAACAGAGAGTGGGAATTCCAAAGTATG	319		
Db	18463	GTCCATTGGACAACAGAGTGGGAATTCCAAAGTAGG	19501		

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RESULT 12
US-09-313-294A-492
; Sequence 492, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 492
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6476212 700549333H1
US-09-313-294A-492

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Query Match	27.5%	Score 90;	DB 4;	Length 301;
Best Local Similarity	74.0%	Pred. No. 4.4e-22;		
Matches 114;	Conservative	0;	Mismatches 40;	Indels 0;
			Gaps	0;

Qy	38	CCACAGCGCGGGGAGAGAGCGCTTTGAAGTCGAAAAGTGGNATCGCATAGCCCTCT	97
Db	146	CCTCTCCGAGACCCACAAAGCGCTTCGAGATCAAGAATGGAAACCGCTCGCGCTCT	205
Qy	98	GGGCTGGGATATTGTGGTTGATTAACGTGTGCATCTGCGAGAAACACATATTGATCTTT	157
Db	206	GGGCATGGGATATCGTCGTGCACAACTGCGGTATCTGCCGCAACACATCATGGATCTAT	265
Qy	158	GCATAGAAATGTCAAGCTAACACAGCGCTCCGGTAC	191
Db	266	GCATCGAGTGCAGCGCAACCAAGCCAGCGCGAC	299

RESULT 13
US-09-836-312A-7
; Sequence 7, Application US/09826312A
; Patent No. 6737244
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Ubiquitin Ligase Assay
; FILE REFERENCE: 021044-00701005
; CURRENT APPLICATION NUMBER: US/09/826,312A
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: RING finger protein ROC2
US-09-826-312A-7

Query Match	22.6%	Score 74;	DB 4;	Length 342;
Best Local Similarity	58.4%	Pred. No. 2.8e-16;		
Matches 153; Conservative	0;	Mismatches 100;	Indels 9;	Gaps 1;

52 GGCAAGAAGCGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGGCCCTGGGATATT 111

76 GGGCAAGAATGTTCTCCCTCAAGAAGTGAACCCGGTGGCCATCTGGAGCTGGGACGTG 139

112 GTGGTGATAAACATGGTCCCATCTCGAGGAGGCCATATATGGATCTTTCATAGAGAGATGCA 177

136 GAGTGCATACGTGCGCCCATCTGAGGGTCCAGGTGATGGATGCCGTGCTCTTACATGTCAA 195

172 GCTAACACAGGCGTCCGCTACTTCAGAAGAGTCTGTCGCATGGGAGTCTCTAACCAT 231

b
196 GCTGAAA-----CAAACAAGAGGACTGTGTTGTGGTCTGGGAGAAATCTAATCAT 246

232 GCTTTTCATTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGAC 291

247 TCCATCCACAACTGCTGCATGTCCCTGTGGTGGAACAGAAACAATCGCTGCCCTCTCTGC 300

252 AACAGAGAGTGGGATTTCCAAA 319
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307 CAGCAGGACTGGGTGGTCCAAA 328

RESULT 14
US-09-542-497A-7
; Sequence 7, Application US/09542497A
; Patent No. 6740495

; GENERAL INFORMATION:
 ; APPLICANT: Issakani, Sarkiz D.
 ; APPLICANT: Huang, Jianing
 ; APPLICANT: Shueng, Julie
 ; TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	616	100.0	482	US-09-513-999C-3894	Sequence 3894, Ap
2	616	100.0	507	US-09-949-016-4940	Sequence 4940, Ap
3	501.5	81.4	3208	US-09-780-016-27	Sequence 27, Appl
4	501.5	81.4	3208	US-10-214-811-27	Sequence 27, Appl
5	479	77.8	411	US-09-640-211A-1731	Sequence 1731, Ap
c	400.5	65.0	490	US-09-270-767-26812	Sequence 26812, A
c	7	400.5	65.0	US-09-270-767-11265	Sequence 11265, A
8	394	64.0	402	US-09-513-999C-10371	Sequence 10371, A
9	394	64.0	463	US-09-621-976-15180	Sequence 15180, A
10	375.5	61.0	357	US-09-248-796A-5495	Sequence 5495, Ap
11	287	46.6	342	US-09-826-312A-7	Sequence 7, Appl
12	287	46.6	342	US-09-542-497A-7	Sequence 7, Appl

13	262.5	42.6	301	4	US-09-313-294A-492	Sequence 492, Appl
14	217	35.2	648	4	US-09-599-360B-27	Sequence 27, Appl
15	200.5	32.5	534	4	US-09-621-976-1817	Sequence 1817, Appl
16	198	32.1	671	4	US-09-621-976-1854	Sequence 1854, Appl
17	197.5	32.1	539	4	US-09-621-976-2051	Sequence 2051, Appl
18	191	31.0	654	4	US-09-621-976-1945	Sequence 1945, Appl
19	175	28.4	25274	4	US-09-949-016-16682	Sequence 16682, A
20	173	28.1	585	4	US-09-270-767-10788	Sequence 10788, A
21	150.5	24.4	439	4	US-09-799-451-296	Sequence 296, Appl
22	146	23.7	170	4	US-09-270-767-26253	Sequence 26253, A
23	91	14.8	940	4	US-09-023-655-667	Sequence 667, Appl
24	91	14.8	1839	4	US-09-828-303-10	Sequence 10, Appl
25	90	14.6	872	4	US-09-774-528-304	Sequence 304, Appl
26	90	14.6	893	4	US-09-949-016-4980	Sequence 4980, Appl
27	90	14.6	1690	4	US-09-828-303-2	Sequence 2, Appl
28	90	14.6	3140	4	US-09-774-528-255	Sequence 255, Appl
29	90	14.6	8438	1	US-07-945-283-1	Sequence 1, Appl
30	88	14.3	1183	4	US-09-799-451-763	Sequence 763, Appl
31	86	14.0	363	4	US-09-640-211A-1319	Sequence 1319, Appl
32	86	14.0	1267	4	US-09-949-016-378	Sequence 378, Appl
33	86	14.0	1267	4	US-09-949-016-2914	Sequence 2914, Appl
34	85.5	13.9	3304	4	US-09-799-451-220	Sequence 220, Appl
35	85	13.8	1621	4	US-09-023-655-20	Sequence 20, Appl
36	85	13.8	1995	4	US-09-949-016-3134	Sequence 3134, Appl
37	85	13.8	2339	3	US-09-268-140-11	Sequence 11, Appl
38	85	13.8	2505	3	US-09-268-140-1	Sequence 1, Appl
39	85	13.8	2517	3	US-09-268-140-7	Sequence 7, Appl
40	85	13.8	15733	4	US-09-949-016-14876	Sequence 14876, A
41	84	13.6	3260	4	US-09-270-767-10326	Sequence 10326, A
42	83.5	13.6	624	4	US-09-270-767-963	Sequence 963, Appl
43	83.5	13.6	624	4	US-09-270-767-16245	Sequence 16245, A
44	83	13.5	315	3	US-09-325-932A-4	Sequence 4, Appl
45	81.5	13.2	4259	2	US-08-816-155B-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-513-999C-3894
; Sequence 3894, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59 US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3894
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 29..352
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 401
; OTHER INFORMATION: r-a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 404
; OTHER INFORMATION: m-a or c
US-09-513-999C-3894

Alignment Scores: 1.7e-69 Length: 482
Pred. No.: 482

Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-513-999C-3894 (1-482)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
DB 29 ATGGCGGACGATGGATGGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 88
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
DB 89 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 148
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuGluCysGlnAlaAsnGln 60
DB 149 AACTGTGCCATCTGCAGGAACCAACATATTATGATCTTTCATAGAAATGTCAAGCTAACACAG 208
QY 61 AlaSerAlaThrSerGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 209 GCGTCGCGTACTTCAGAGAGTGTACTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 268
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 269 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACACAGAGAG 328
QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 329 TGGGAATTCAAAAGTATGGGCAC 352

RESULT 2
US-09-949-016-4940
; Sequence 4940, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4940
; LENGTH: 507
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4940

Alignment Scores:
Pred. No.: 1,82e-69 Length: 507
Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-949-016-4940 (1-507)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
DB 7 ATGGCGGACGATGGATGGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 66
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40

DB 67 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 126
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuGluCysGlnAlaAsnGln 60
DB 127 AACTGTGCCATCTGCAGGAACCAACATATTATGATCTTTCATAGAAATGTCAAGCTAACACAG 186
QY 61 AlaSerAlaThrSerGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 187 GCGTCGCGTACTTCAGAGAGTGTACTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 246
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 247 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACACAGAGAG 306
QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 307 TGGGAATTCAAAAGTATGGGCAC 330

RESULT 3
US-09-780-016-27
; Sequence 27, Application US/09780016
; Patent No. 6509456
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6509456el Human Proteases and
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/09/780,016
; PRIOR FILING DATE: 2001-02-09
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-780-016-27

Alignment Scores:
Pred. No.: 1,03e-53 Length: 3208
Score: 501.50 Matches: 88
Percent Similarity: 95.70% Conservative: 1
Best Local Similarity: 94.62% Mismatches: 1
Query Match: 81.41% Indels: 3
DB: 4 Gaps: 1

US-09-541-462B-2 (1-108) x US-09-780-016-27 (1-3208)

QY 16 GlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrp 35
DB 2752 GGAGCATATAAAAAAAAAA-----AAAAATGGAATGCAGTAGACCTCTGGGCTGG 2802
QY 36 AspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuGluGlu 55
DB 2803 GATATTGTGTGTGATTAACCTGTCCATCTGCAGGAACCAACATATTATGATCTTTTCATAGAA 2862
QY 56 CysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCys 75
DB 2863 TGTCAAGCTAACAGCGCGCTACTTCAGAGAGTGTACTGTCATGGGAGTCTGT 2922
QY 76 AsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCysPro 95
DB 2923 AACCATGCTTTTCACCTTCCATCTCTCGCTGCATCTCTCGCTGCCTCAAAACACGACAGGTGTGTCCA 2982
QY 96 LeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis 108

```

; CURRENT APPLICATION NUMBER: US/09/640,211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1731
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Pinus radiata
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(411)
; OTHER INFORMATION: n = A,T,C or G
US-09-640-211A-1731

Alignment Scores:
Pred. No.: 4,28e-52 Length: 411
Score: 479.00 Matches: 90
Percent Similarity: 84.96% Conservative: 6
Best Local Similarity: 79.65% Mismatches: 4
Query Match: 77.76% Indels: 13
DB: Gaps: 3

US-09-541-462B-2 (1-108) x US-09-640-211A-1731 (1-411)
QY 3 AlaAlaMetAspValAsp-----ThrProSer-----GlyThrAsnSerGlyAla 17
Db 74 GCTTCAACAGACATAGATATGTTCCGTCGCCCTCTGGCGAGGGTTCCAGCTCTCAAGCG 133
QY 18 Gly-----LysLysArgPheGluValLysLysThrAsnAlaVal 30
Db 134 GGACCAAGCGTTCACCAGAGGCCAAAGTTTCGAAATCAAGAAGTGGAATGCTGTA 193
QY 31 AlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 194 GCCCTTTGGCGTGGGATATTGTGTTGATAATTGTGCAATTTGCAGAAACCATCATG 253
QY 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
Db 254 GACCTCTGTATTGAGTGTGAGGCAAAATCAAGCAAGTGCAACAAGTGAAGAATGTACTGTT 313
QY 71 AlaTrpGlyValCysAsnHisAlaPheHisCysIleSerArgTrpLeuLysThr 90
Db 314 GCATGGGGGTGTTGCAATCACGCTTTTCATTTCATTGCATAAAGTCGGTGGCTCAAGACA 373
QY 91 ArgGlnValCysProLeuAspAsnArg-GluTrpGlu 102
Db 374 CGACAAAGTCTGCCCATAGATAATAAGTGAGTGGAG 410

RESULT 6
US-09-270-767-26812/c
; Sequence 26812, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26812
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-26812

Alignment Scores:
Pred. No.: 5,82e-42 Length: 490
Score: 400.50 Matches: 70
Percent Similarity: 77.57% Conservative: 13
Best Local Similarity: 65.42% Mismatches: 19
Query Match: 65.02% Indels: 5
DB: Gaps: 2

```


Db 261 AAGTATGGGCAC 272

RESULT 9

US-09-621-976-15180

; Sequence 15180, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054P2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 15180

; LENGTH: 463

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 74

; OTHER INFORMATION: n=a, g, c or t

US-09-621-976-15180

Alignment Scores:

Pred. No.: 3,63e-41 Length: 463

Score: 394.00 Matches: 76

Percent Similarity: 73.08% Conservative: 0

Best Local Similarity: 73.08% Mismatches: 2

Query Match: 63.96% Indels: 27

DB: 4 Gaps: 1

US-09-541-462B-2 (1-108) x US-09-621-976-15180 (1-463)

QY 5 MetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysIleValArgPheGluVal 24

DB 35 ATGGATGTGGATACCCGAGCGGCCCAACACGCGCGCGGCCGAGCGCTTTGAAGTG 94

QY 25 LysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIle 44

DB 95 AAAAAGGC----- 102

QY 45 CysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThr 64

DB 103 -----ATAGAATGTCAAGCTAACCGCGCTCCGCTACT 135

QY 65 SerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisCysIle 84

DB 136 TCAGAAGAGTGTACTGTGCGCATGGGGAGTCTGTAAACCATGCTTTTCACTTCCACTGCATC 195

QY 85 SerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGln 104

DB 196 TCTCCTGCTCTAAACACGACGAGGTGTGTCTTATTTGGACACAGAGATGGGAATTCAC 255

QY 105 LysTrpGlyHis 108

DB 256 AAGTATGGGCAC 267

RESULT 10

US-09-248-796A-5495

; Sequence 5495, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; LENGTH: 357

; TYPE: DNA

; ORGANISM: Candida albicans

US-09-248-796A-5495

Alignment Scores:

Pred. No.: 5,82e-39 Length: 357

Score: 375.50 Matches: 62

Percent Similarity: 73.27% Conservative: 12

Best Local Similarity: 61.39% Mismatches: 26

Query Match: 60.96% Indels: 1

DB: 4 Gaps: 1

US-09-541-462B-2 (1-108) x US-09-248-796A-5495 (1-357)

QY 9 ThrProSerGlyThrAsnSerGlyAlaGlyLysIleValArgPheGluValLysLysTrpAsn 28

DB 52 ACAACAGAACCAACATCAAAACCAACCATCAAAACCAACAGATTGGAAGTGAAGAAATGGACA 111

QY 29 AlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHis 48

DB 112 GCGGTAGCGTTTGTCTATGGATATGCAAAATGAAAATTTGCCATTTGTAGAATCAT 171

QY 49 IleMetAspLeuCysIleGluCysGlnAlaAsn---GlnAlaSerAlaThrSerGluGlu 67

DB 172 TTAATGGAACCATGATTGAATGTCAACCAATGCTATGATATTTCCCTTCAGAGAG 231

QY 68 CysThrValAlaTrpGlyValCysAsnHisAlaPheHisCysIleSerArgTrp 87

DB 232 TGTATTCCTGCTGGGAGTATGTAATCATGCTATTTACATTTGATTAGAAAGATGG 291

QY 88 LeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGly 107

DB 292 TTGAACACAGAAATGCTATGCTTGGATAGTACTAATTTGGACTTATCAAAATTTGGGT 351

QY 108 His 108

DB 352 AAT 354

RESULT 11

US-09-826-312A-7

; Sequence 7, Application US/09826312A

; Patent No. 6737244

; GENERAL INFORMATION:

; APPLICANT: Issakani, Sarkiz D.

; APPLICANT: Huang, Jianing

; APPLICANT: Sheung, Julie

; APPLICANT: Pray, Todd R.

; APPLICANT: Rigel Pharmaceuticals, Inc.

; TITLE OF INVENTION: Ubiquitin Ligase Assay

; FILE REFERENCE: 021044-007010US

; CURRENT APPLICATION NUMBER: US/09/826,312A

; CURRENT FILING DATE: 2001-04-03

; PRIOR APPLICATION NUMBER: US 09/542,497

; PRIOR FILING DATE: 2000-04-03

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: Patentin ver. 2.1

; SEQ ID NO 7

; LENGTH: 342

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: RING finger protein ROC2

US-09-826-312A-7

Alignment Scores:

Pred. No.: 1.1e-27 Length: 342

Score: 287.00 Matches: 48

Percent Similarity: 63.92% Conservative: 14

```
Best Local Similarity: 49.48% Mismatches: 31
Query Match: 46.59% Indels: 4
DB: 4 Gaps: 2

US-09-541-462B-2 (1-108) x US-09-826-312A-7 (1-342)
QY 11 SerGlyThrAsnSerGlyAlaGlyLysLysAspPheGluValLysLysTrpAsnAlaVal 30
DB 58 TCAGGCTCAACGTCGGA---GGCGACAGATGTTCTCCCTCAAGAAGTGGAAACCCGGTG 114
QY 31 AlaLeuTrpAlaTrpAspLeuValValAspAsnCysAlaIleCysArgAsnHisIleMet 50
DB 115 GCCATGTGGAGTGGGACGTGGAGTACGATACGTGGCCATCTGCAGGGTCCAGGTGATG 174
QY 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
DB 175 GATGCTGTCTTAGATGTCAAGCTGAAAC-----AAACAAGAGGACTGTGTTGTG 225
QY 71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr 90
DB 226 GTCTGGGAGAGTATATCTTCCTCCACAACGTGCTGATGCTCCCTGTGGTGAACAG 285
QY 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGly 107
DB 286 AACAAATCGCTGCTCTGCCAGCAGGACTGGTGGTCCAAAGAATCGGC 336

RESULT 12
US-09-542-497A-7
; Sequence 7, Application US/09542497A
; Patent No. 6740495
; GENERAL INFORMATION:
; APPLICANT: Isaakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Shuang, Julie
; TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY
; FILE REFERENCE: A-68613/RMS/JJD
; CURRENT APPLICATION NUMBER: US/09/542,497A
; CURRENT FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 342
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-542-497A-7

Alignment Scores:
Pred. No.: 1,1e-27 Length: 342
Score: 287.00 Matches: 48
Percent Similarity: 63.92% Conservative: 14
Best Local Similarity: 49.48% Mismatches: 31
Query Match: 46.59% Indels: 4
DB: 4 Gaps: 2

US-09-541-462B-2 (1-108) x US-09-542-497A-7 (1-342)
QY 11 SerGlyThrAsnSerGlyAlaGlyLysLysAspPheGluValLysLysTrpAsnAlaVal 30
DB 58 TCAGGCTCAACGTCGGA---GGCGACAGATGTTCTCCCTCAAGAAGTGGAAACCCGGTG 114
QY 31 AlaLeuTrpAlaTrpAspLeuValValAspAsnCysAlaIleCysArgAsnHisIleMet 50
DB 115 GCCATGTGGAGTGGGACGTGGAGTACGATACGTGGCCATCTGCAGGGTCCAGGTGATG 174
QY 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70
DB 175 GATGCTGTCTTAGATGTCAAGCTGAAAC-----AAACAAGAGGACTGTGTTGTG 225
QY 71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThr 90
DB 226 GTCTGGGAGAGTATATCTTCCTCCACAACGTGCTGATGCTCCCTGTGGTGAACAG 285
QY 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrGly 107

Best Local Similarity: 49.48% Mismatches: 31
Query Match: 46.59% Indels: 4
DB: 4 Gaps: 2

US-09-541-462B-2 (1-108) x US-09-313-294A-492 (1-301)
QY 3 AlaAlaMetAspValAsp-----ThrProSerGlyThrAsnSer 15
DB 70 TCCGCCATGGAGACCGACATCAAGCGCGCGCGCCGCCAGCTGGCGAGGATCC 129
QY 16 GlyAlaGly-----LysLysArgPheGluValLysLysTrp 27
DB 130 TCTGCGCGCGTCCGTCCTCTCCCAAGCCCAACAAAGCGCTTCGAGATCAAGAAGTGG 189
QY 28 AsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAlaIleCysArgAsn 47
DB 190 AACGCCGTGCGCTCTGGCGATGGGATATCGTCTGCACTGCGCTATCTGCCGCAAC 249
QY 48 HisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThr 64
DB 250 CACATCATGATCTATGATCGAGTCCAGGCGCAACCAAGCCAGCGCGACC 300

RESULT 14
US-09-599-360B-27
; Sequence 27, Application US/09599360B
; Patent No. 6548633
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bougueleret, L.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: GENSET.050CP3
; CURRENT APPLICATION NUMBER: US/09/599,360B
; CURRENT FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/141,032
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 09/469,099
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent.pm
; SEQ ID NO 27
```

```
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 187..438
; NAME/KEY: polyA_signal
; LOCATION: 612..617
; NAME/KEY: polyA_site
; LOCATION: 632..648
US-09-599-360B-27
Alignment Scores:
Pred. No.: 2,368-18 Length: 648
Score: 217.00 Matches: 43
Percent Similarity: 44.53% Conservative: 18
Best Local Similarity: 31.39% Mismatches: 40
Query Match: 35.23% Indels: 36
DB: 4 Gaps: 3
US-09-541-462B-2 (1-108) x US-09-599-360B-27 (1-648)
Qy 2 AlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyValAlaGlyLysLysArg 21
Db 49 GCCGCGACTGTGGTCTTTTATACCTTCCCGCGGACGCGCGCTGCCAACGGAAGG 108
Qy 22 PheGlu-----PheGluValLysLysTrpAsnAlaValAlaLeuTrpAla 34
Db 109 GCGGAGACGGAGTTTCGTATGTTGCCAGGCCCATTTGAGATCTTTGAAGATATCTCA 168
Qy 24 -----ValLysLysTrpAsnAlaValAlaLeuTrp 33
Db 169 ACGTGAGGCTCTGCTGCCATGAGTGAGATTAAAGTCTGGAACGGCGTGCCACTTGG 228
Qy 34 AlaTrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCys 53
Db 229 CTCCTGGTGGCCACAGATGAGAACTGTGGCATCTGCAGGATGGCATTAAACGGATGCTG 288
Qy 54 IleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGly 73
Db 289 CTGACTGCAAG-----GTGCCCGGCGACGACTGCCGCTGTGTGGGGC 333
Qy 74 ValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnVal 93
Db 334 CAGTGCTCCCACTGCTTCCACATGATTCATTCCTCAAGTGGCTGCACGACGAGGTG 393
Qy 94 -----CysProLeuAspAsnArgGluTrpGluPheGlnLysTyrgly 107
Db 394 CAGCAGCACTGCCCATGTGCGCCAGGAGTGAAGTTCAAGGAGTGAGGC 444
RESULT 15
US-09-621-976-1817
; Sequence 1817, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1817
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 106..441
; NAME/KEY: sig_peptide
; LOCATION: 106..423
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.40000009536743
; OTHER INFORMATION: seq GILILLPHAGADG/CW
US-09-621-976-1817
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Pred. No.: 2,368-16 Length: 534
Score: 200.50 Matches: 42
Percent Similarity: 51.72% Conservative: 18
Best Local Similarity: 36.21% Mismatches: 41
Query Match: 32.55% Indels: 16
DB: 4 Gaps: 3
US-09-541-462B-2 (1-108) x US-09-621-976-1817 (1-534)
Qy 2 AlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArg 21
Db 31 GCCGCGACTGTGGTCTTTTATACCTTCCCGCGGACGCGCGCTGCCAACGGAAGG 90
Qy 22 -----PheGluValLysLysTrpAsnAlaValAlaLeuTrpAla 34
Db 91 GCGGGCTCTGCTGCCATGAAGTGAAGATTAAAGTCTGGAACGGCGTCCCACTTGGCTC 150
Qy 35 TrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIle 54
Db 151 TGGTGGCCACGATGAGAACTGTGGCATCTGCAGGATGGCATTAAACGGATGCTGCCCT 210
Qy 55 GluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGlyVal 74
Db 211 GACTGCAAG-----GTGCCCGGCGACGACTGCCGCTGTGTGGGGCCAG 255
Qy 75 CysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnVal---- 93
Db 256 TGCTCCCACTGCTTCCACATGCAATTCCTCAAGTGGCTGCACGACGACGAGGTGCAG 315
Qy 94 -----CysProLeuAspAsnArgGluTrpGluPheGlnLysTyrgly 107
Db 316 CAGCACTGCCCATGTGCGGCCA-GAATGGAAGTTCAAGGAGTGAGGC 362
Search completed: June 24, 2005, 12:05:35
Job time : 159 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2005, 15:20:31 ; Search time 43 Seconds
(without alignments)
187.491 Million cell updates/sec

Title: US-09-541-462B-2
Perfect score: 616
Sequence: 1 MAAMDVDTSGTNSGAGKK.....KTRQVCPLDNREWEFKYGH 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	616	100.0	108	4	US-09-826-312A-6
2	616	100.0	108	4	US-09-542-497A-6
3	616	100.0	108	4	US-09-513-999C-7971
4	616	100.0	110	4	US-09-949-016-10811
5	375.5	61.0	118	4	US-09-248-796A-19598
6	287	46.6	113	4	US-09-826-312A-8
7	287	46.6	113	4	US-09-542-497A-8
8	208	33.8	84	4	US-09-599-360B-77
9	202	32.8	84	4	US-09-826-312A-5
10	202	32.8	84	4	US-09-542-497A-5
11	185	30.0	112	4	US-09-621-976-5677
12	185	30.0	112	4	US-09-621-976-5805
13	105.5	17.1	94	4	US-09-621-976-5714
14	90	14.6	195	4	US-09-949-016-10851
15	86	14.0	326	4	US-09-949-016-6249
16	86	14.0	336	4	US-09-949-016-8785
17	85	13.8	664	3	US-09-268-140-2
18	85	13.8	664	4	US-09-949-016-9005
19	84	13.6	556	4	US-09-270-767-41922
20	83.5	13.6	181	4	US-09-270-767-32592
21	83.5	13.6	181	4	US-09-270-767-47809
22	83	13.5	104	4	US-09-325-932A-49
23	83	13.5	337	4	US-09-828-303-18
24	81	13.1	484	4	US-09-248-796A-15483
25	80.5	13.1	895	4	US-09-270-767-42746
26	80	13.0	160	4	US-09-949-016-8123
27	80	13.0	180	2	US-08-786-606-3

28	80	13.0	180	2	US-08-933-750C-48	Sequence 48, Appl
29	80	13.0	180	3	US-09-234-613-48	Sequence 48, Appl
30	80	13.0	180	4	US-09-949-016-11029	Sequence 11029, A
31	80	13.0	252	4	US-09-270-767-45203	Sequence 45203, A
32	80	13.0	284	2	US-08-786-606-9	Sequence 9, Appl
33	79	12.8	50	3	US-09-052-089A-15	Sequence 15, Appl
34	79	12.8	114	4	US-09-270-767-57487	Sequence 57487, A
35	79	12.8	352	4	US-09-270-767-42211	Sequence 42211, A
36	79	12.8	359	4	US-09-663-600A-106	Sequence 106, App
37	79	12.8	381	2	US-08-867-057-1	Sequence 1, Appl
38	79	12.8	381	2	US-08-867-057-3	Sequence 3, Appl
39	79	12.8	381	2	US-09-128-369-1	Sequence 1, Appl
40	79	12.8	381	2	US-09-128-369-3	Sequence 3, Appl
41	79	12.8	381	4	US-09-663-600A-200	Sequence 200, App
42	79	12.8	410	1	US-07-945-283-4	Sequence 4, Appl
43	78	12.7	448	4	US-09-949-016-9938	Sequence 9938, Ap
44	77.5	12.6	342	4	US-09-270-767-45316	Sequence 45316, A
45	77	12.5	258	4	US-09-949-016-9556	Sequence 9556, Ap

ALIGNMENTS

RESULT 1

US-09-826-312A-6
; Sequence 6, Application US/09826312A
; Patent No. 6737244
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: Ubiquitin Ligase Assay
; FILE REFERENCE: 021044-007010US
; CURRENT APPLICATION NUMBER: US/09/826,312A
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: RING finger protein ROC1

Query Match 100.0%; Score 616; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.7e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAAMDVDTSGTNSGAGKKRFEVKKNVALWAWD1VVDNCAICRNHIMDLCTECQANQ	60
Db	1	MAAMDVDTSGTNSGAGKKRFEVKKNVALWAWD1VVDNCAICRNHIMDLCTECQANQ	60
Qy	61	ASATSECTVAVGVCNHAFFHCISRWLKTRQVCPLDNREWEFKYGH	108
Db	61	ASATSECTVAVGVCNHAFFHCISRWLKTRQVCPLDNREWEFKYGH	108

RESULT 2

US-09-542-497A-6
; Sequence 6, Application US/09542497A
; Patent No. 6740495
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY
; FILE REFERENCE: A-68613/RMS/JJD
; CURRENT APPLICATION NUMBER: US/09/542,497A

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; CURRENT FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-542-497A-6

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Query Match	100.0%	Score 616;	DB 4;	Length 108;
Best Local Similarity	100.0%	Pred. No. 4,7e-60;		
Matches 108;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 MAAAMDVDTPSGTNSGAGKKRFEVKKNVALWAWDI VVDNCAICRNHIMDLCECQANQ 60

Db 1 MAAAMDVDTPTSGTNSGAGKKRFEVKKNVALWAWDIWVNCACRNHIMDLCECOANO 60

QY 61 ASATSEECTVAWGVCNHAFFHFCISRWLKTRQVCPLDNREWEFFQKYGH 108

61 ASATSEECTVAWGVCNHAFFHFCISRWLKTROVCPLDNREWEFFQKYGH 108

RESULT 3

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US-09-513-999C-7971
; Sequence 7971, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,48
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 7971
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-7971

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Query Match	100.0%	Score 616;	DB 4;	Length 108;
Best Local Similarity	100.0%	Pred. No. 4,7e-60;		
Matches 108:	Conservative	0;	Mismatches 0;	Indels 0;
	Gaps	0;		

1 MAAAMPDVTPTSGTNSGAGKKRFEVKKNVALWAWDI VPDNCAICRNHIMDLCECOANO 60

db

QY 61 ASATSEECTVAWGVCNHAFFHFCISRWLKTROVCPLDNREWEFFQKYGH 108

61 ASATSEECTVANGVCNHAFFHFHCISRWLKTROVCPLDNREWEFOKYGH 108

RESULT 4

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US-09-949-016-10811
; Sequence 10811, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOW
; TITLE OF INVENTION: WITH HUMAN DISEASE,
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03

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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10811
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10811

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Query Match	100.0%;	Score 616;	DB 4;	Length 110;
Best Local Similarity	100.0%;	Pred. No. 4.8e-60;		
Matches 108; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCECQANQ 60

3 MAAAMDVDTPSGTNSGAGKKRFEVKKWNAVALWAWDIVVDNCAICRNHIMDLCECQANQ 62

61 ASATSEECTVANGVCNHAFFHFCISRWLKTROVCPLDNREWEFQKYGH 108 Qv

63 ASATSEECTVAWGVCNHAFFHFCISRWLKTRQVCPLDNREWEFFQKYGH 110

RESULT 5

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US-09-248-796A-19598
; Sequence 19598, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID ANALYSIS FOR DIAGNOSTICS AND ANTICANCER THERAPY
; TITLE OF INVENTION: FOR DIAGNOSTICS AND ANTICANCER THERAPY
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.7
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19598
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19598

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Query Match	61.0%;	Score 375.5;	DB 4;	Length 118;
Best Local Similarity	61.4%;	Pred. No. 1.1e-33;		
Matches 62: Conservative	12;	Mismatches 26;	Indels 1;	Gaps 1;

9 TPSG TNSGAGKURFEVKKNVALWAWDI VVDNCAICRNHIMDL CIECOAN-OASATSEE 67

db 18 TTEPTSKPSSKPRFEVKKWTAVAFWSWDMQIENCAICRNHLMPECI ECOPNAMGNIPSEE 77

QY 68 CTVANGVCNHAFFHFCISRWLKTRQVCPLDNREWEFQKYGH 108

78 CIPAWGVCNHAFFHLHCIRRWLKTENA C P L D S T N W T Y O K L G N 118

RESULT 6

```

US-09-826-312A-8
; Sequence 8, Application US/09826312A
; Patent No. 6737244
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Ubiquitin Ligase Assay
; FILE REFERENCE: 021044-007010US
; CURRENT APPLICATION NUMBER: US/09/826, 312A
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497

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; CURRENT FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 84
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-542-497A-5

```

Query Match	32.8%;	Score 202;	DB 4;	Length 84;
Best Local Similarity	36.4%;	Pred. No. 7.4e-15;		
Matches	32; Conservative	17; Mismatches	31; Indels	8; Gaps 2;
Qy	21	RFEVKKNAVALWAWD1VWNCAICRNHIMDLCTIECQAQASATSECTVAGVCNIAFH	80	
	:	:::	:::	:::
	:	:::	:::	:::
	:	:::	:::	:::
Db	2	KVKIKCWGVATLWLVANDENCIGCRMFGCCPDCK----	VPGDDCPVLWGQCSCHF	56
Qy	81	FHCISRWLKTRQV----	CPLONREWEFOK	105
	:	:::	:::	:::
	:	:::	:::	:::
Db	57	MHCILKWLAHOAOOHCPCMCROTWKFFE	84	

RESULT 11
 US-09-621-976-5677
 ; Sequence 5677, Application US/09621976
 ; Patent No. 6639063
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Jobert, S.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 ; FILE REFERENCE: GENSET.054PR2
 ; CURRENT APPLICATION NUMBER: US/09/621,976
 ; CURRENT FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 19335
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 5677
 ; LENGTH: 112
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SIGNAL
 ; LOCATION: -106...-1
 US-09-621-976-5677

Query Match	30.0%	Score 185;	DB 4;	Length 112;
Best Local Similarity	38.0%;	Pred. No. 7.4e-13;		
Matches	30;	Conservative 13;	Mismatches 28;	Indels 8; Gaps 2;
Qy	21	RFEVKKNAVALMAWDIVDNCATCRNHIMDLCTEQANQASATSEECTVANGVCNHFH	80	
		: : : : : : :		
Db	2	KVKIKCNGVATLWLVANDENCIGICRMAFNCCPDCK----	VPGDDCPLVWGQCSHCF	56
Qy	81	FHCISRWLKTRQV----	CPL 96	
Db	57	MHCITLKWTHAQOVOOHCPM	75	

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RESULT 12
US-09-621-976-5805
; Sequence 5805, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5805

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; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -109...-1
US-09-621-976-5805
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Query Match      30.0%; Score 185; DB 4; Length 112;
Best Local Similarity 38.0%; Pred. No. 7.4e-13;
Matches 30; Conservative 13; Mismatches 28; Indels 8; Gaps 2;

Qy 21 RFEVKGNVAALWANDIVDNCIALCRNHIMDLICIEQANQASATSECTVAGVGNHAPH 80
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 KVKIKCWNGVATLWLVANDENCIGCRMAFNCCPDCK-----VPGDDCLPLVWQCSCHFH 56

Qy 81 FHCISRWLKTRQV---CPL 96

Db 57 MHCILKWLHAAQVOOHCPM 75

```

```

RESULT 13
US-09-621-976-5714
; Sequence 5714, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5714
; LENGTH: 94
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -53...-1
; NAME/KEY: UNSURE
; LOCATION: 14
; OTHER INFORMATION: xaa = Glu,Gln
US-09-621-976-5714

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Query Match	17.1%	Score 105.5;	DB 4;	Length 94;
Best Local Similarity	36.6%;	Pred. No. 0.00031;		
Matches 15; Conservative	8; Mismatches 13; Indels 5; Gaps 1;			
Qy	48	HIMDLICIECOANASATSEECTVAVGVCNHAFFHCISRWL	88	
Dd	10	HLTDAAPDK- - - - VPGDDCLPLVWGOCSCFPMHGIKWL	45	

RESULT 14
US-09-949-016-10851
; Sequence 10851, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10851
 ; LENGTH: 195
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-10851

Query Match 14.6%; Score 90; DB 4; Length 195;
 Best Local Similarity 26.3%; Pred. No. 0.034;
 Matches 25; Conservative 11; Mismatches 15; Indels 44; Gaps 4;
 QY 10 PSRTNSGAGK-----KREPVKKNAVALWADIVDNCNCAICRNHIMDLICIEQANQASAT 64
 DB 23 PSSSNGAGESGGQSTFE-----CNICLDTAKDAVI----- 54
 QY 65 SEECTVAMGVCNHFHFCISRWLKT---RQVCPL 96
 DB 55 -----SLCGHLFCWPCCLHQWLETRPNRQVCPV 81

RESULT 15
 US-09-949-016-6249
 ; Sequence 6249, Application US/09949016
 ; Patent No. 6812319
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6249
 ; LENGTH: 326
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-6249

Query Match 14.0%; Score 86; DB 4; Length 326;
 Best Local Similarity 30.2%; Pred. No. 0.17;
 Matches 19; Conservative 11; Mismatches 23; Indels 10; Gaps 2;
 QY 43 AICRNHIMDLICIEQANQASATSEECTVAMGVCNHFHFCISRWLKTRQVCPLDNREWE 102
 DB 266 AVSRNPLCTCLE-ERRHPTATP-----CGHLFCWECITAWCSSKAECPLCKRKFP 315
 QY 103 FOK 105
 DB 316 PQK 318

Search completed: June 23, 2005, 15:31:18
 Job time : 44 secs

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GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2005, 15:15:21 ; Search time 162 Seconds
(without alignments)
257.840 Million cell updates/sec

Title: US-09-541-462B-2
Perfect score: 616
Sequence: 1 MAAMDVTPSGTNSGAGKK.....KTRQVCPLDREWFQKYGH 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqp1990a:.*
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4: Geneseqp2001a:.*
5: Geneseqp2002a:.*
6: Geneseqp2003a:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004a:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	616	100.0	108	3	AAB08813 A human c
3	616	100.0	108	3	AAG03890 Human sec
4	616	100.0	108	4	AAB47599 ROC1. 1/2
5	616	100.0	108	5	AAB24620 Human RIN
6	616	100.0	108	7	ADC02481 RING fing
7	616	100.0	108	7	ADF17866 RING fing
8	616	100.0	108	8	ABM82365 Tumour-as
9	616	100.0	108	8	ADSB8291 Human pro
10	534	86.7	108	4	ABB68080 Drosophil
11	514.5	83.5	118	3	AGC23004 Arabidops
12	511	83.0	109	3	AGC23005 Arabidops
13	400.5	65.0	122	4	ABE66109 Drosophil
14	385	62.5	121	3	AAB08814 A yeast c
15	336	54.5	59	8	ADP22560 Sea-squir
16	323	52.4	57	3	AAB41007 Human ORF
17	292	47.4	113	2	AAY06492 Human sen
18	292	47.4	113	3	AAB43295 Human ORF
19	292	47.4	113	8	ADR97346 Human RNF
20	292	47.4	118	4	AAU15873 Human nov
21	292	47.4	118	6	ABU54942 Human nov
22	292	47.4	131	4	AAU16332 Human nov
23	292	47.4	131	6	ABU55401 Human nov
24	291	47.2	113	2	AAY06509 Human sen
25	290.5	47.2	113	2	AAY06491 Mouse sen

26	290.5	47.2	113	3	AAB19161	Aab19161 Amino aci
27	287	46.6	113	4	AAB47600	Aab47600 ROC2. 1/2
28	287	46.6	113	5	AAE24621	Aae24621 Human RIN
29	287	46.6	113	7	ADC02483	Adc02483 RING fing
30	287	46.6	113	7	ADF17868	Adf17868 RING fing
31	285	46.3	113	2	AAY06508	Aay06508 Human sen
32	283	45.9	113	2	AAY06500	Aay06500 Human sen
33	283	45.9	113	2	AAU08501	Aay06501 Human sen
34	282	45.8	113	2	AAY06496	Aay06496 Human sen
35	282	45.8	113	2	AAU06503	Aay06503 Human sen
36	282	45.8	113	2	AAY06502	Aay06502 Human sen
37	282	45.8	113	2	AAY06506	Aay06506 Human sen
38	282	45.8	113	2	AAY06495	Aay06495 Human sen
39	282	45.8	113	2	AAU06499	Aay06499 Human sen
40	282	45.8	113	2	AAY06498	Aay06498 Human sen
41	282	45.8	113	2	AAU06505	Aay06505 Human sen
42	274	44.5	113	2	AAY06504	Aay06504 Human sen
43	272	44.2	113	2	AAY06497	Aay06497 Human sen
44	272	44.2	113	2	AAY06507	Aay06507 Human sen
45	255.5	41.5	100	8	ADP22582	Adp22582 Sea-squir

ALIGNMENTS

RESULT 1
AAB19160
ID AAB19160 standard; protein; 108 AA.
XX
AC AAB19160;
XX
DT 19-FEB-2001 (first entry)
XX
DE Amino acid sequence of human ring finger protein ROC1.
XX
KW ROC1; ROC2; cullin; ring finger protein; APC11; APC complex; SCF pathway;
KW cullin dependent ubiquitin ligase; CDK inhibitor Sic1 degradation;
KW tumour.
XX
OS Homo sapiens.
XX
PN WO200058472-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US008592.
XX
PR 31-MAR-1999; 99US-0127261P.
XX
PR 22-NOV-1999; 99US-0166927P.
XX
(UYNC-) UNIV NORTH CAROLINA.
XX
Xiong Y, Ohta T;
XX
WPI; 2000-647235/62.
XX
N-PSDB; AAA96882.
XX
Novel nucleic acid encoding cullin regulating ring finger proteins,
XX
termed as ROC proteins similar to anaphase-promoting complex 11, for
XX
therapeutic and diagnostic use.
XX
Claim 9; Fig 2A; 83pp; English.
XX
The present sequence represents a human ROC1 ring finger protein. The
XX
specification also describes human ROC2, ROC1 and ROC2 are similar to
XX
APC11, a subunit of the APC complex. The proteins stimulate cullin
XX
dependent ubiquitin ligase activity. ROC1 functions in vivo as an
XX
essential regulator of CDK inhibitor Sic1 degradation by the SCF
XX
(undefined) pathway. ROC proteins are useful for screening bioactive
XX
agents that interfere with the binding of ROC proteins with cullin
XX
proteins. Pharmaceutical formulations comprising ROC proteins are useful
XX
for diagnostic and therapeutic purposes, preferably for diagnosing and
XX
treating tumours

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 616; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.8e-64;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAAMDVDTPSGTNSGAGKRRFEVKKNNAVALWAWMDIVVDNCAICRNHIMDLICIEQANQ 60
DB 1 MAAAMDVDTPSGTNSGAGKRRFEVKKNNAVALWAWMDIVVDNCAICRNHIMDLICIEQANQ 60

QY 61 ASATSECTVAMGVCNHAFFHCHISRWLKTRQVCPDLDNREWEFQKYGH 108
DB 61 ASATSECTVAMGVCNHAFFHCHISRWLKTRQVCPDLDNREWEFQKYGH 108

RESULT 2
AAB08813
ID AAB08813 standard; protein; 108 AA.

XX AC AAB08813;
XX DT 02-JAN-2001 (first entry)
XX DE A human cullin-interacting RING-H2 finger protein (Rbx1).
XX KW Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;
XX KW tumour suppressor; carcinoma; Ring box associated carcinoma;
XX KW von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;
XX KW cerebellar hemangioblastoma; hemangioma; retinal angiomata;
XX KW pheochromocytomas.
XX OS Homo sapiens.
XX WO200050445-A1.
XX 31-AUG-2000.
XX 25-FEB-2000; 2000WO-US004838.
XX 26-FEB-1999; 99US-0121787P.
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX PA Conaway JA, Conaway RC, Kamura T;
XX PI Conaway JA, Conaway RC, Kamura T;
XX WPI; 2000-572067/53.
XX N-PSDB; AAA74978.

XX CC Cullin interacting RING-H2 finger protein, a component of von Hippel-Lindau tumor suppressor complex and Skp1-Cdc53p-F-box protein (SCF)
XX PT ubiquitin ligase, useful for diagnosing and treating Ring box protein associated carcinomas.
XX PS Claim 1; Page 34; 37pp; English.

XX CC The present sequence represents a human cullin-interacting RING-H2 finger protein (Ring box protein), designated Rbx1. The polypeptide is a tumour suppressor. Rbx1 is useful for diagnosing a predisposition of a patient to certain carcinomas. It is also useful for treating Ring box protein associated carcinomas or augmenting metabolically deficient system in animals. Rbx1 is also useful for evaluating the effectiveness of a therapeutic treatment for Ring box associated carcinomas. Rbx1 can be used to screen for agents which augment or inhibit the activity of other cullin-containing ubiquitin ligase and of the VHL (von Hippel-Lindau) complex controlling the conjugation of ubiquitin or ubiquitin-like proteins to various sets of target proteins. Carcinomas which may be treated include renal carcinomas, cerebellar hemangioblastomas and hemangiomas, retinal angiomata and pheochromocytomas

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 616; DB 3; Length 108;

Best Local Similarity 100.0%; Pred. No. 3.8e-64;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAAMDVDTPSGTNSGAGKRRFEVKKNNAVALWAWMDIVVDNCAICRNHIMDLICIEQANQ 60
DB 1 MAAAMDVDTPSGTNSGAGKRRFEVKKNNAVALWAWMDIVVDNCAICRNHIMDLICIEQANQ 60

QY 61 ASATSECTVAMGVCNHAFFHCHISRWLKTRQVCPDLDNREWEFQKYGH 108
DB 61 ASATSECTVAMGVCNHAFFHCHISRWLKTRQVCPDLDNREWEFQKYGH 108

RESULT 3
AAG03890
ID AAG03890 standard; protein; 108 AA.

XX AC AAG03890;
XX DT 06-OCT-2000 (first entry)
XX DE Human secreted protein, SEQ ID NO: 7971.
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KW gene therapy; chromosome mapping.
XX OS Homo sapiens.
XX EP1033401-A2.
XX PD 06-SEP-2000.
XX PF 21-FEB-2000; 2000EP-00200610.
XX PR 26-FEB-1999; 99US-0122487P.
XX (GEST) GENSET.
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
XX N-PSDB; AAC03896.

XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX PS Claim 13; SEQ ID NO 7971; 71pp + Sequence Listing; English.

XX CC The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors

XX SQ Sequence 108 AA;

Query Match 100.0%; Score 616; DB 3; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.8e-64;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAAMDVDTPSGTNSGAGKRRFEVKKNNAVALWAWMDIVVDNCAICRNHIMDLICIEQANQ 60
DB 1 MAAAMDVDTPSGTNSGAGKRRFEVKKNNAVALWAWMDIVVDNCAICRNHIMDLICIEQANQ 60

QY 61 ASATSECTVAMGVCNHAFFHCHISRWLKTRQVCPDLDNREWEFQKYGH 108

Db 61 ASATSECTVAGVNCNHAFFHCISRWLKTRQVCPDLNREWEFKYGH 108
|||||

RESULT 4
AAB47599
ID AAB47599 standard; protein; 108 AA.
XX AAB47599;
AC AAB47599;
DT 07-JAN-2002 (first entry)
XX ROC1.
DE
XX
KW Assay; ubiquitin ligase; tag1-ubiquitin; E1; E2;
KW ubiquitin activating enzyme; ubiquitin conjugating enzyme; E3;
KW ubiquitin ligase; ubiquitination modulator.
XX Unidentified.
OS
XX WO200175145-A2.
PN
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US010906.
XX
PR 03-APR-2000; 2000US-00542497.
XX
PA (RIGE-) RIGEL PHARM INC.
XX
PI Issakani SD, Huang J, Sheung J, Pray TR;
XX
XX WPI; 2001-626445/72.
DR
XX
XX
PT Assaying ubiquitin ligase activity for identifying modulators of
PT ubiquitination, by combining ubiquitin, ubiquitin activating conjugating
PT enzyme, ubiquitin ligase and measuring amount of ubiquitin bound to the
PT ligase.
XX
XX Example 1; Fig 11; 98pp; English.
PS
XX
XX The sequences given in AAB47596-602 are proteins which may be used in the
XX method of the invention for assaying ubiquitin ligase activity. The
XX method comprises combining under conditions that favour ubiquitin ligase
XX activity, tag1-ubiquitin, E1 (ubiquitin activating enzyme), E2 (ubiquitin
XX conjugating enzyme) and E3 (ubiquitin ligase) and measuring the amount of
XX tag1-ubiquitin bound to the E3. The method is useful for assaying
XX ubiquitin ligase activity and ubiquitination enzyme activity which is
XX useful for identifying ubiquitination modulator. The method comprises
XX combining tag1-ubiquitin, the modulator, E1, E2 and tag2-E3 and measuring
XX the amount of tag1-ubiquitin bound to tag2-E3 or combining tag1-
XX ubiquitin, modulator, E1 and tag3-E2 and measuring the amount of tag1-
XX ubiquitin bound to tag3-E2. Ubiquitin ligase activity is measured
XX directly, eliminating the need for target proteins and subsequent
XX analysis such as separating ligated from unligated material in an SDS-
XX PAGE procedure. This allows multi-well array analysis and high throughput
XX screening techniques for modulators of ubiquitination activity. The
XX method also allows the analysis of many different combinations of E3
XX components and E2/E3 combinations without requiring prior identification
XX of specific target substrates. Ubiquitin is labeled, directly or
XX indirectly and this allows for easy and rapid detection and measurement
XX of ligated ubiquitin
XX Sequence 108 AA;
Query Match 100.0%; Score 616; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.8e-64;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAAAMDVDTPSGTNSGAGKRFEVKKNNAVALWAWDIVVDNCAICRNHMDLCIECQANQ 60
Db 1 MAAAMDVDTPSGTNSGAGKRFEVKKNNAVALWAWDIVVDNCAICRNHMDLCIECQANQ 60
|||||

Qy 61 ASATSECTVAGVNCNHAFFHCISRWLKTRQVCPDLNREWEFKYGH 108
|||||

Db 61 ASATSECTVAGVNCNHAFFHCISRWLKTRQVCPDLNREWEFKYGH 108
|||||

RESULT 5
AAE24620
ID AAE24620 standard; protein; 108 AA.
XX
AC AAE24620;
XX
DT 22-OCT-2002 (first entry)
XX
XX Human RING finger protein, ROC1.
DE
XX Ubiquitin ligase; UL; tag1-ubiquitin; E1; ubiquitin-activating enzyme;
KW E2; ubiquitin-conjugating enzyme/ubiquitin carrier protein; E3; human;
KW RING finger protein.
XX
OS Homo sapiens.
XX
XX US2002042083-A1.
PN
XX
PD 11-APR-2002.
XX
PF 03-APR-2001; 2001US-00826312.
XX
PR 03-APR-2000; 2000US-00542497.
XX
PA (RIGE-) RIGEL PHARM INC.
XX
PI Issakani SD, Huang J, Sheung J, Pray TR;
XX
XX WPI; 2002-488718/52.
DR
XX
XX Assay for ubiquitin ligase activity, useful for identifying modulators,
PT by measuring binding of labeled ubiquitin to ubiquitin ligase.
XX
XX Disclosure; Fig 11; 56pp; English.
PS
XX
XX The invention relates to an assay for ubiquitin ligase (UL) activity
CC which comprises incubating tag1-ubiquitin, E1 (ubiquitin-activating
CC enzyme), E2 (ubiquitin-conjugating enzyme/ubiquitin carrier protein) and
CC E3 (UL) and measuring the amount of tag1-ubiquitin bound to E3. The
CC method is particularly used to screen for modulators of UL activity. The
CC present sequence is human RING finger protein, ROC1
XX
XX Sequence 108 AA;
Query Match 100.0%; Score 616; DB 5; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.8e-64;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MAAAMDVDTPSGTNSGAGKRFEVKKNNAVALWAWDIVVDNCAICRNHMDLCIECQANQ 60
Db 1 MAAAMDVDTPSGTNSGAGKRFEVKKNNAVALWAWDIVVDNCAICRNHMDLCIECQANQ 60
|||||

Qy 61 ASATSECTVAGVNCNHAFFHCISRWLKTRQVCPDLNREWEFKYGH 108
|||||

Db 61 ASATSECTVAGVNCNHAFFHCISRWLKTRQVCPDLNREWEFKYGH 108
|||||

RESULT 6
ADC02481
ID ADC02481 standard; protein; 108 AA.
XX
AC ADC02481;
XX
DT 18-DEC-2003 (first entry)
XX
XX RING finger protein ROC1.
DE
XX
XX ubiquitin; Mdm2; p53; RING finger protein; ROC1.
KW

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XX OS Unidentified.
XX PN US2003104474-A1.
XX PD 05-JUN-2003.
XX PF 26-MAR-2002; 2002US-00108767.
XX PF 03-APR-2000; 2000US-00542487.
XX PR 03-APR-2001; 2001US-00826312.
XX PR 04-MAR-2002; 2002US-00091139.
XX PA (ISSA/) ISSAKANI S D.
XX PA (HUAN/) HUANG J.
XX PA (SHEU/) SHEUNG J.
XX PA (PRAY/) PRAY T R.
XX PI Issakani SD, Huang J, Sheung J, Pray TR;
XX WPI; 2003-787056/74.
XX DR Assaying for candidate agent that modulates attachment of ubiquitin
XX PT moiety to Mdm2 protein comprises combining ubiquitin agent comprising
XX PT ubiquitin moiety, Mdm2 protein, and candidate agent.
XX PS Disclosure; Fig 11; 96pp; English.
XX SS The present sequence represents a method of assaying for a candidate
XX CC agent that modulates the attachment of a ubiquitin moiety to an Mdm2
XX CC protein. The method is useful for assaying for a candidate agent that
XX CC modulates the attachment of a ubiquitin moiety to an Mdm2 or p53 protein.
XX CC The present sequence represents the amino acid sequence of RING finger
XX CC protein ROC1.
XX CC Sequence 108 AA;
XX SQ
Query Match 100.0%; Score 616; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.8e-64;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAMADVDTFSGTNSGAGKKRFEVKKNAVALWAWDIVVDNCAICRNHIMDLCEQANQ 60
DB 1 MAAMADVDTFSGTNSGAGKKRFEVKKNAVALWAWDIVVDNCAICRNHIMDLCEQANQ 60
QY 61 ASATSEECTVAMGVNCNHAFFHCISRWLKTRQVCPLDNREWEFQKYGH 108
DB 61 ASATSEECTVAMGVNCNHAFFHCISRWLKTRQVCPLDNREWEFQKYGH 108
RESULT 7
ADFI7866
ID ADFI7866 standard; protein; 108 AA.
XX AC ADFI7866;
XX DT 12-FEB-2004 (first entry)
XX DE RING finger protein ROC1, an E3 ubiquitin ligating agent.
XX KW ROC1; ubiquitin-mediated proteolysis; high-throughput screening;
XX KW E3 ubiquitin ligating agent; RING finger.
XX OS Unidentified.
XX PN US2003108947-A1.
XX PD 12-JUN-2003.
XX PF 20-MAY-2002; 2002US-00152156.
XX PR 03-APR-2000; 2000US-00542497.
XX PR 03-APR-2001; 2001US-00826312.
PR 18-MAY-2001; 2001US-0291836P.
PR 04-MAR-2002; 2002US-00091139.
PR 04-MAR-2002; 2002US-00091174.
PR 26-MAR-2002; 2002US-00108767.
PR 26-MAR-2002; 2002US-00109460.
XX (ISSA/) ISSAKANI S D.
XX PA (HUAN/) HUANG J.
XX PA (SHEU/) SHEUNG J.
XX PA (PRAY/) PRAY T R.
XX PI Issakani SD, Huang J, Sheung J, Pray TR;
XX WPI; 2003-810851/76.
XX DR Assaying agent that modulates attachment of ubiquitin moiety to
XX PT ubiquitin agent, by combining first ubiquitin agent, candidate agent and
XX PT ubiquitin moiety, and assaying agent.
XX PS Disclosure; Fig 11; 95pp; English.
XX SS This invention relates to a novel method for assaying ubiquitin agents
XX CC that are enzymatic components of ubiquitin-mediated proteolysis.
XX CC Specifically, it refers to a method for identifying ubiquitin-activating,
XX CC -conjugating and -ligating agents that work to modulate the attachment of
XX CC ubiquitin moiety to at least one other ubiquitin agent. The method
XX CC comprises combining a first ubiquitin agent, candidate agent and
XX CC ubiquitin moiety, and subsequently assaying for the attachment of a
XX CC ubiquitin moiety to the first agent. The present invention does not
XX CC require a ubiquitin target protein and allows the analysis of many
XX CC different combinations of ubiquitin agents, without requiring the
XX CC identification of specific target proteins. Consequently, this method is
XX CC easy, applicable for high-throughput screening applications and so can
XX CC rapidly detect the activity of ubiquitin agents. This polypeptide
XX CC sequence is the RING finger protein ROC1, an E3 ubiquitin ligating agent
XX CC of the invention.
XX CC Sequence 108 AA;
XX SQ
Query Match 100.0%; Score 616; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 3.8e-64;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAMADVDTFSGTNSGAGKKRFEVKKNAVALWAWDIVVDNCAICRNHIMDLCEQANQ 60
DB 1 MAAMADVDTFSGTNSGAGKKRFEVKKNAVALWAWDIVVDNCAICRNHIMDLCEQANQ 60
QY 61 ASATSEECTVAMGVNCNHAFFHCISRWLKTRQVCPLDNREWEFQKYGH 108
DB 61 ASATSEECTVAMGVNCNHAFFHCISRWLKTRQVCPLDNREWEFQKYGH 108
RESULT 8
ABM82365
ID ABM82365 standard; protein; 108 AA.
XX AC ABM82365;
XX DT 18-NOV-2004 (first entry)
XX DE Tumour-associated antigenic target (TAT) polypeptide PRO83289, SEQ:6073.
XX KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX KW tumour; diagnosis; cell proliferative disorder; breast cancer;
XX KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
XX KW central nervous system cancer; bladder cancer; pancreatic cancer;
XX KW cervical cancer; melanoma; leukaemia; hybridisation probe;
XX KW chromosome identification; chromosome mapping; gene mapping;
XX KW gene therapy; cytostatic.
XX OS Homo sapiens.
XX PN WO2004030615-A2.

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XX Drosophila melanogaster.
OS WO200171042-A2.
PN
XX
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX PF
XX 23-MAR-2000; 2000US-0191637P.
XX PR
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX DR
XX N-PSDB; ABL12183.
XX
XX
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
XX Disclosure; SEQ ID NO 31032; 21pp + Sequence Listing; English.
XX
XX PS
XX CC The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 108 AA;

Query Match 86.7%; Score 534; DB 4; Length 108;
Best Local Similarity 87.2%; Pred. No. 1.6e-54;
Matches 95; Conservative 4; Mismatches 4; Indels 6; Gaps 2;

QY 5 MDYD-----TPSGTNSGAKKREVKKNNAVALWAWDI VVDNCAICRNHIMDL CIECQAN 59
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 1 MEVDEDCGYEVPSSSSKG-DKKREVKKNNAVALWAWDI VVDNCAICRNHIMDL CIECQAN 59
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY 60 QASATSEECTVANGVNCNHAFPHFCISRWLKTRQVCPDLNREWFQKYGH 108
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 60 QASATSEECTVANGVNCNHAFPHFCISRWLKTRQVCPDLNREWFQKYGH 108
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 11
AAG23004
ID AAG23004 standard; protein; 118 AA.
XX
XX AC AAG23004;
XX
XX DT 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 26148.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
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PR 13-JUL-1999;	99US-0143542P.	PR 04-OCT-1999;	99US-0157117P.
PR 14-JUL-1999;	99US-0143624P.	PR 05-OCT-1999;	99US-0157753P.
PR 15-JUL-1999;	99US-0144005P.	PR 06-OCT-1999;	99US-0157865P.
PR 16-JUL-1999;	99US-0144086P.	PR 07-OCT-1999;	99US-0158029P.
PR 17-JUL-1999;	99US-0144086P.	PR 08-OCT-1999;	99US-0158232P.
PR 18-JUL-1999;	99US-0144325P.	PR 09-OCT-1999;	99US-0158369P.
PR 19-JUL-1999;	99US-0144331P.	PR 10-OCT-1999;	99US-0158369P.
PR 19-JUL-1999;	99US-0144332P.	PR 11-OCT-1999;	99US-0159293P.
PR 19-JUL-1999;	99US-0144332P.	PR 12-OCT-1999;	99US-0159293P.
PR 19-JUL-1999;	99US-0144333P.	PR 13-OCT-1999;	99US-0159294P.
PR 19-JUL-1999;	99US-0144333P.	PR 13-OCT-1999;	99US-0159295P.
PR 19-JUL-1999;	99US-0144333P.	PR 14-OCT-1999;	99US-0159329P.
PR 20-JUL-1999;	99US-0144335P.	PR 14-OCT-1999;	99US-0159330P.
PR 20-JUL-1999;	99US-0144352P.	PR 14-OCT-1999;	99US-0159331P.
PR 20-JUL-1999;	99US-0144632P.	PR 14-OCT-1999;	99US-0159637P.
PR 20-JUL-1999;	99US-0144884P.	PR 14-OCT-1999;	99US-0159638P.
PR 21-JUL-1999;	99US-0144884P.	PR 18-OCT-1999;	99US-0159584P.
PR 21-JUL-1999;	99US-0145086P.	PR 21-OCT-1999;	99US-0160741P.
PR 21-JUL-1999;	99US-0145088P.	PR 21-OCT-1999;	99US-0160767P.
PR 22-JUL-1999;	99US-0145087P.	PR 21-OCT-1999;	99US-0160768P.
PR 22-JUL-1999;	99US-0145087P.	PR 21-OCT-1999;	99US-0160770P.
PR 22-JUL-1999;	99US-0145088P.	PR 21-OCT-1999;	99US-0160814P.
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Best Local Similarity 78.6%; Pred. No. 3.5e-52;

Matches 92; Conservative 6; Mismatches 8; Indels 11; Gaps 2;

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AC AAG23005;

XX 17-OCT-2000 (first entry)

DT

XX Arabidopsis thaliana protein fragment SEQ ID NO: 26149.

DE Protein identification; signal transduction pathway; metabolic pathway;

XX hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

XX Arabidopsis thaliana.

OS

XX EPI033405-A2.

PN

XX 06-SEP-2000.

PD

XX 25-FEB-2000; 2000EP-00301439.

PF

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XX 05-MAR-1999; 99US-0123180P.

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PR 28-OCT-1999; 99US-0161922P.
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Best Local Similarity 88.8%; Pred. No. 8.1e-52;
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XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX Drosophila melanogaster.
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XX WO200171042-A2.
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XX 27-SEP-2001.
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XX 23-MAR-2001; 2001WO-US009231.
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XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX (PEKE) PE CORP NY.
PA Venter JC, Adams M, Li PWD, Myers EW;
PI
XX

DR WPI; 2001-656860/75.
DR N-PSDB; ABL10212.
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PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
XX
PS Disclosure; SEQ ID NO 25119; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
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SQ Sequence 122 AA;
Query Match 65.0%; Score 400.5; DB 4; Length 122;
Best Local Similarity 65.4%; Pred. No. 8.7e-39;
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DB 75 PNANQDECTVANGVCNHAFFHCISRWLKTRQVCPLDNREWEFQYKG 121

RESULT 14
AAB08814
ID AAB08814 standard; protein; 121 AA.
XX AAB08814;
XX 02-JAN-2001 (first entry)
XX A yeast cullin-interacting RING-H2 finger protein (Rbx1).
DE Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;
KW tumour suppressor; carcinoma; Ring box associated carcinoma;
KW von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;
KW cerebellar hemangioblastoma; hemangioma; retinal angiomas;
KW pheochromocytomas.
XX Saccharomyces cerevisiae.
XX WO200050445-A1.
PN 31-AUG-2000.
PD 25-FEB-2000; 2000WO-US004838.
PF 26-FEB-1999; 99US-0121787P.
PR (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX Conaway JA, Conaway RC, Kamura T;
PI
XX WPI; 2000-572067/53.
DR N-PSDB; AAA74979.
XX Cullin interacting RING-H2 finger protein, a component of von Hippel-
PT Lindau tumor suppressor complex and Skp1-Cdc53p-F-box protein (SCF)
PT ubiquitin ligase, useful for diagnosing and treating Ring box protein
PT associated carcinomas.
XX

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2005, 15:29:52 ; Search time 158 Seconds
(without alignments)
262.856 Million cell updates/sec

Title: US-09-541-462B-2

Perfect score: 616
Sequence: 1 MAAMDVDTSGTSGAGKK.....KTRQVCPLDNRWFQKYGH 108

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	616	100.0	108	9	US-09-826-312-6
2	616	100.0	108	14	US-10-108-767-6
3	616	100.0	108	14	US-10-152-156-6
4	616	100.0	108	17	US-10-913-937-1
5	616	100.0	108	17	US-10-835-096-6
6	534	86.7	108	17	US-10-913-937-6
7	524	85.1	124	15	US-10-767-701-43736
8	518.5	84.2	118	15	US-10-424-599-148916
9	512	83.1	109	16	US-10-425-115-201494
10	512	83.1	111	16	US-10-767-701-43735
11	506.5	82.2	152	15	US-10-424-599-221431

12	493	80.0	110	17	US-10-913-937-7	Sequence 7, Appli
13	420.5	68.3	106	15	US-10-424-599-148915	Sequence 148915,
14	420	68.2	82	16	US-10-425-115-191492	Sequence 191492,
15	420	68.2	97	16	US-10-425-115-291051	Sequence 291051,
16	385	62.5	121	17	US-10-913-937-2	Sequence 2, Appli
17	356.5	57.9	98	16	US-10-425-115-352839	Sequence 352839,
18	313	50.8	75	15	US-10-424-599-230014	Sequence 230014,
19	308.5	50.1	132	16	US-10-425-115-336213	Sequence 336213,
20	294.5	47.8	109	16	US-10-767-701-51814	Sequence 51814, A
21	292	47.4	118	9	US-09-764-864-826	Sequence 826, App
22	292	47.4	131	9	US-09-764-864-1285	Sequence 1285, Ap
23	287	46.6	64	15	US-10-424-599-238320	Sequence 238320,
24	287	46.6	113	9	US-09-826-312-8	Sequence 8, Appli
25	287	46.6	113	14	US-10-108-767-8	Sequence 8, Appli
26	287	46.6	113	14	US-10-152-156-8	Sequence 8, Appli
27	287	46.6	113	17	US-10-835-096-8	Sequence 8, Appli
28	282	45.8	68	15	US-10-424-599-242288	Sequence 242288,
29	228	37.0	40	15	US-10-424-599-264079	Sequence 264079,
30	213	34.6	88	9	US-09-925-298-620	Sequence 620, App
31	213	34.6	88	14	US-10-102-806-620	Sequence 620, App
32	213	34.6	88	15	US-10-276-774-2678	Sequence 2678, Ap
33	213	34.6	91	15	US-10-264-049-2937	Sequence 2937, Ap
34	213	34.6	105	9	US-09-764-864-1274	Sequence 1274, Ap
35	210	34.1	124	9	US-09-764-864-1284	Sequence 1284, Ap
36	208	33.8	84	11	US-09-978-3603-409	Sequence 409, App
37	208	33.8	84	15	US-10-315-664-77	Sequence 77, Appli
38	208	33.8	84	15	US-10-221-625-94	Sequence 94, Appli
39	208	33.8	100	15	US-10-424-599-253860	Sequence 253860,
40	203	33.0	84	16	US-10-767-701-51781	Sequence 51781, A
41	202	32.8	84	9	US-09-826-312-5	Sequence 5, Appli
42	202	32.8	84	14	US-10-108-767-5	Sequence 5, Appli
43	202	32.8	84	14	US-10-152-156-5	Sequence 5, Appli
44	202	32.8	84	17	US-10-835-096-5	Sequence 5, Appli
45	196	31.8	85	15	US-10-264-049-2926	Sequence 2926, Ap

ALIGNMENTS

RESULT 1

US-09-826-312-6
; Sequence 6, Application US/09826312
; Patent No. US20020042083A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: UBIQUITIN LIGASE ASSAY
; FILE REFERENCE: A-68613-1/RMS/JJD
; CURRENT APPLICATION NUMBER: US/09/826,312
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-312-6

Query Match	100.0%	Score 616;	DB 9;	Length 108;
Best Local Similarity	100.0%	Pred. No. 7.7e-60;		
Matches 108;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	61	ASATSEECTVAGVCNHAFFHCISRLWKTQVCPDNRWFQKYGH	108	

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US-10-108-767-6
; Sequence 6, Application US/10108767
; Publication No. US2003010474A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS AND FOR IDENTIFYING AGENTS
; FILE OF INVENTION: MODIFY THE ACTIVITY OF UBIQUITIN AGENTS
; FILE REFERENCE: A-68613-5/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/108,767
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 10/091,139
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-767-6

Query Match 100.0%; Score 616; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 7,7e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 ASATSEECTVAMGVNCNHAHFHCHISRWLKTRQVCPLDNREWEFQKYGH 108

RESULT 3
US-10-152-156-6
; Sequence 6, Application US/10152156
; Publication No. US20030108947A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: ASSAYS FOR IDENTIFYING UBIQUITIN AGENTS AND FOR IDENTIFYING AGENTS
; FILE OF INVENTION: MODIFY THE ACTIVITY OF UBIQUITIN AGENTS
; FILE REFERENCE: A-68613-6/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/152,156
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 10/091,174
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 10/091,139
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 10/109,460
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 10/108,767
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: US 60/291,836
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
US-10-152-156-6

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Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ASATSEECTVAMGVNCNHAHFHCHISRWLKTRQVCPLDNREWEFQKYGH 108
DB 61 ASATSEECTVAMGVNCNHAHFHCHISRWLKTRQVCPLDNREWEFQKYGH 108

RESULT 4
US-10-913-937-1
; Sequence 1, Application US/10913937
; Publication No. US20050019813A1
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Kamura, Takumi
; APPLICANT: Okanoma Medical Research Foundation
; TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor
; FILE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/10/913,937
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: US/09/914,324
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human ring box protein 1 (Rbx1)
US-10-913-937-1

Query Match 100.0%; Score 616; DB 17; Length 108;
Best Local Similarity 100.0%; Pred. No. 7,7e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ASATSEECTVAMGVNCNHAHFHCHISRWLKTRQVCPLDNREWEFQKYGH 108
DB 61 ASATSEECTVAMGVNCNHAHFHCHISRWLKTRQVCPLDNREWEFQKYGH 108

RESULT 5
US-10-835-096-6
; Sequence 6, Application US/10835096
; Publication No. US20050032139A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: Ubiquitin Ligase Assay
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; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-152-156-6

Query Match 100.0%; Score 616; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 7,7e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MAAAMDVTPSGTNSGAGKRRFEVKKNAVALWAWDIVVDNCAICRNHMDLCIECQANQ 60
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RESULT 4
US-10-913-937-1
; Sequence 1, Application US/10913937
; Publication No. US20050019813A1
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Kamura, Takumi
; APPLICANT: Okanoma Medical Research Foundation
; TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor
; FILE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/10/913,937
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: US/09/914,324
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human ring box protein 1 (Rbx1)
US-10-913-937-1

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Best Local Similarity 100.0%; Pred. No. 7,7e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ASATSEECTVAMGVNCNHAHFHCHISRWLKTRQVCPLDNREWEFQKYGH 108
DB 61 ASATSEECTVAMGVNCNHAHFHCHISRWLKTRQVCPLDNREWEFQKYGH 108

RESULT 5
US-10-835-096-6
; Sequence 6, Application US/10835096
; Publication No. US20050032139A1
; GENERAL INFORMATION:
; APPLICANT: Issakani, Sarkiz D.
; APPLICANT: Huang, Jianing
; APPLICANT: Sheung, Julie
; APPLICANT: Pray, Todd R.
; TITLE OF INVENTION: Ubiquitin Ligase Assay
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; FILE REFERENCE: 021044-007010US
; CURRENT APPLICATION NUMBER: US/10/835,096
; CURRENT FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US/09/826,312
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 09/542,497
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: RING finger protein ROC1
US-10-835-096-6

Query Match      100.0%; Score 616; DB 17; Length 108;
Best Local Similarity 100.0%; Pred. No. 7.7e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAAMDVTPSGTNSGAGKRFVKKNNAVALWAWDIIVDNCACRNHMDLCIECOANQ 60
Db 1 MAAAMDVTPSGTNSGAGKRFVKKNNAVALWAWDIIVDNCACRNHMDLCIECOANQ 60

QY 61 ASATSEECTVAVGVCNHAHFHCISRWLKTRQVCPLDNRWEFQKYGH 108
Db 61 ASATSEECTVAVGVCNHAHFHCISRWLKTRQVCPLDNRWEFQKYGH 108

RESULT 6
US-10-913-937-6
; Sequence 6, Application US/10913937
; Publication No. US20050019813A1
; GENERAL INFORMATION:
; APPLICANT: Conaway, Jean A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklahoma Medical Research Foundation
; TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/10/913,937
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: US/09/914,324
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Drosophila melanogaster ring box protein 1 (Rbx1)
US-10-913-937-6

Query Match      86.7%; Score 534; DB 17; Length 108;
Best Local Similarity 87.2%; Pred. No. 8.1e-51;
Matches 95; Conservative 4; Mismatches 4; Indels 6; Gaps 2;

QY 5 MDVD-----TPSGTNSGAGKRFVKKNNAVALWAWDIIVDNCACRNHMDLCIECOAN 59
Db 1 MEVDDGGEVPSSSKSG-DKGRFEVKKNNAVALWAWDIIVDNCACRNHMDLCIECOAN 59

QY 60 QASATSEECTVAVGVCNHAHFHCISRWLKTRQVCPLDNRWEFQKYGH 108
Db 60 QASATSEECTVAVGVCNHAHFHCISRWLKTRQVCPLDNRWEFQKYGH 108
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RESULT 7
US-10-767-701-43736
; Sequence 43736, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 43736
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB5052-011-A1-XP1-A5.pep
US-10-767-701-43736

Query Match      85.1%; Score 524; DB 16; Length 124;
Best Local Similarity 90.9%; Pred. No. 1.2e-49;
Matches 90; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 10 PSGTNSGAGKRFVKKNNAVALWAWDIIVDNCACRNHMDLCIECOANQASATSECT 69
Db 26 PSSSTSRKPKRFEIKKNNAVALWAWDIIVDNCACRNHMDLCIECOANQASATSECT 85

QY 70 VAVGVCNHAHFHCISRWLKTRQVCPLDNRWEFQKYGH 108
Db 86 VAVGVCNHAHFHCISRWLKTRQVCPLDNRWEFQKYGH 124

RESULT 8
US-10-424-599-148916
; Sequence 148916, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 148916
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_105494C.1.pep
US-10-424-599-148916

Query Match      84.2%; Score 518.5; DB 15; Length 118;
Best Local Similarity 80.3%; Pred. No. 4.5e-49;
Matches 94; Conservative 5; Mismatches 7; Indels 11; Gaps 3;

QY 3 AAMDVDT---PSG-TNSGAG-----KKRFEVKKNNAVALWAWDIIVDNCACRNHMD 51
Db 2 ATLDSDVTVPAGEASSSSSTKKPKRFEIKKNNAVALWAWDIIVDNCACRNHMD 61

QY 52 LCIECOANQASATSEECTVAVGVCNHAHFHCISRWLKTRQVCPLDNRWEFQKYGH 108
Db 62 LCIECOANQASATSEECTVAVGVCNHAHFHCISRWLKTRQVCPLDNRWEFQKYGH 118

RESULT 9
US-10-425-115-201494
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; Sequence 201494, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201494
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_115346C.1.pep
US-10-425-115-201494

Query Match      83.1%; Score 512; DB 16; Length 109;
Best Local Similarity 85.6%; Pred. No. 2.1e-48;
Matches 89; Conservative 4; Mismatches 9; Indels 2; Gaps 1;

QY 7 VDTSGTNSGAG--KRFEVKKNAVALWAWDIVVDNCAICRNHMDLCIECOANQASAT 64
Db 6 VVPPAPAAAKAKRFEIKKNVSLWAWDIVVDNCAICRNHMDLCIECOANQASAT 65
QY 65 SEECTVAMGVCNHAHFHFCISRWLKTRQVCPDLNREWEFQKYGH 108
Db 66 SEECTVAMGVCNHAHFHFCISRWLKTRQVCPDLNREWEFQKYGH 109

RESULT 10
US-10-767-701-43735
; Sequence 43735, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 43735
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C17809_1.pep
US-10-767-701-43735

Query Match      83.1%; Score 512; DB 16; Length 111;
Best Local Similarity 91.7%; Pred. No. 2.2e-48;
Matches 88; Conservative 4; Mismatches 2; Indels 2; Gaps 1;

QY 15 SGAGK--KRFEVKKNAVALWAWDIVVDNCAICRNHMDLCIECOANQASATSEECTVAM 72
Db 16 AAGKAKAFDICKWNAVSLWAWDIVVDNCAICRNHMDLCIECOANQASATSEECTVAM 75
QY 73 GVCNHAHFHFCISRWLKTRQVCPDLNREWEFQKYGH 108
Db 76 GVCNHAHFHFCISRWLKTRQVCPDLNREWEFQKYGH 111

RESULT 11
US-10-424-599-221431
; Sequence 221431, Application US/10424599
; Publication No. US20040031072A1
```

```
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 221431
; LENGTH: 152
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_41982C.1.pep
US-10-424-599-221431

Query Match      82.2%; Score 506.5; DB 15; Length 152;
Best Local Similarity 80.0%; Pred. No. 1.2e-47;
Matches 92; Conservative 4; Mismatches 10; Indels 9; Gaps 2;

QY 3 AAMDVDTP-----SGTNSGAG-----KGRFEVKKNAVALWAWDIVVDNCAICRNHMDLC 53
Db 38 ATLDSVPMVPAGEPSSSSAGSSSKPKRFEIKKNNAVALWAWDIVVDNCAICRNHMDLC 97
QY 54 IECQANQASATSEECTVAMGVCNHAHFHFCISRWLKTRQVCPDLNREWEFQKYGH 108
Db 98 IECQANQASATSEECTVAMGVCNHAHFHFCISRWLKTRQVCPDLNREWEFQKYGH 152

RESULT 12
US-10-913-937-7
; Sequence 7, Application US/10913937
; Publication No. US20050019813A1
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklamoma Medical Research Foundation
; TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/10/913,937
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: US/09/914,324
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; OTHER INFORMATION: Caenorhabditis elegans ring box protein 1 (Rbx1)
US-10-913-937-7

Query Match      80.0%; Score 493; DB 17; Length 110;
Best Local Similarity 79.3%; Pred. No. 2.7e-46;
Matches 88; Conservative 5; Mismatches 14; Indels 4; Gaps 2;

QY 1 MAQAAMD---VDTPSGTNSGAGKKRFEVKKNAVALWAWDIVVDNCAICRNHMDLCIECO 57
Db 1 MAQASDSTAMEVEEATNTQTV--KGRFEVKKSAVALWAWDIQVDNCAICRNHMDLCIECO 59
QY 58 ANQASATSEECTVAMGVCNHAHFHFCISRWLKTRQVCPDLNREWEFQKYGH 108
Db 60 ANQAAGLKDECTVAMGVCNHAHFHFCISRWLKTRQVCPDLNREWEFQKYGH 110
```


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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 23, 2005, 15:19:51 ; Search time 39 Seconds
(without alignments)
266.446 Million cell updates/sec

Title: US-09-541-462B-2
Perfect score: 616
Sequence: 1 MAAAMDVDTSGTNSGAGKK.....KTRQVCPDNRWEFQKYGH 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	616	100.0	108	2 T51146	ring-box protein 1
2	510	82.8	136	2 T13388	hypothetical prote
3	499	81.0	115	2 T47341	ring-box protein-1
4	493	80.0	110	2 T27823	hypothetical prote
5	469	76.1	107	2 T38310	pop-interacting pr
6	385	62.5	121	2 S68830	hypothetical prote
7	378	61.4	166	2 T18513	hypothetical prote
8	266	43.2	112	2 T29620	hypothetical prote
9	164.5	26.7	94	2 T38652	hypothetical prote
10	146.5	23.8	135	2 T21802	hypothetical prote
11	136	22.1	165	2 S2511	hypothetical prote
12	132.5	21.5	99	2 G30113	Rbp1 protein [limp
13	116.5	18.9	2160	2 T20241	hypothetical prote
14	104	16.9	349	2 T06680	hypothetical prote
15	102.5	16.6	249	2 C96775	probable RING zinc
16	102	16.6	210	2 T45654	zinc-finger-like p
17	100	16.2	676	2 T47637	hypothetical prote
18	97	15.7	159	2 T48209	hypothetical prote
19	97	15.7	327	2 D86474	probable RING zinc
20	96	15.6	332	2 E86448	hypothetical prote
21	95.5	15.5	441	2 F71425	hypothetical prote
22	95	15.4	253	2 T06113	hypothetical prote
23	95	15.4	322	2 H85474	hypothetical prote
24	95	15.4	336	2 T28358	ORF MSV197 tryptop
25	95	15.4	362	2 T51464	RING-H2 zinc finger
26	95	15.4	530	2 T50499	hypothetical prote
27	95	15.4	689	2 F84811	probable retroelem
28	92	14.9	185	2 T51844	RING-H2 finger pro
29	91.5	14.9	190	2 T51859	

Query Match 82.8%; Score 510; DB 2; Length 136;

RESULT 1

T51146
ring-box protein 1 [imported] - human
C:Species: Homo sapiens (man)
C>Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
C:Accession: T51146
R:Kamura, T.; Koopp, D.M.; Conrad, M.N.; Skowrya, D.; Moreland, R.J.; Iliopoulos, O.; Lar
Science 284, 657-661, 1999
A:Title: Rbx1, a component of the VHL tumor suppressor complex and SCF ubiquitin ligase.
A:Reference number: 225317; MUID:99234320; PMID:10213691
A:Accession: T51146
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-108 <KAM>
A:Cross-references: UNIPROT:Q8N6Z8; EMBL:AF140598; PIDN:AAD29715.1
C:Genetics:
A:Gene: RBX1

Query Match 100.0%; Score 616; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 9.9e-59;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAAMDVDTSGTNSGAGKKRFEVKWNAVALWAWDIIVVDNCAICRNHIMDLCECQANQ 60
Db 1 MAAAMDVDTSGTNSGAGKKRFEVKWNAVALWAWDIIVVDNCAICRNHIMDLCECQANQ 60
Qy 61 ASATSECTVAMGVCNHAHAFHCISRWLKTRQVCPDNRWEFQKYGH 108
Db 61 ASATSECTVAMGVCNHAHAFHCISRWLKTRQVCPDNRWEFQKYGH 108

RESULT 2

T13388
hypothetical protein 115C2.11 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13388
R:Salles, C.; Valenti, P.; Darlamitsou, A.; Henderson, N.; Campbell, L.; Glover, D.
submitted to the EMBL Data Library, May 1999
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: Z17665
A:Accession: T13388
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-136 <CAT>

A:Cross-references: UNIPROT:Q9W5E1; EMBL:AL031581; PIDN:CAA20888.1
C:Genetics:
A:Cross-references: FlyBase:FBgn020381
A:Introns: 64/1
A>Note: EG:115C2.11

Query Match 82.8%; Score 510; DB 2; Length 136;

30 91.5 14.9 496 2 B96674
31 91.5 14.9 571 2 T40911
32 91 14.8 530 2 T28366
33 90.5 14.7 677 2 T39713
34 90 14.6 213 2 T14811
35 90 14.6 532 2 T49467
36 90 14.6 1208 2 T05077
37 89.5 14.5 202 2 T06621
38 89.5 14.5 624 2 T01585
39 89 14.4 357 2 E85092
40 89 14.4 456 2 T19377
41 88.5 14.4 336 2 A86406
42 88.5 14.4 524 2 P96572
43 88 14.3 141 2 S15788
44 88 14.3 161 2 E88541
45 88 14.3 200 2 T41745

ALIGNMENTS

hypothetical prote
probable PHD-type
ORF MSV205 tryptop
zinc finger protei
hypothetical prote
related to COP1-in
hypothetical prote
hypothetical prote
probable RING zinc
hypothetical prote
hypothetical prote
probable RING zinc
protein F12M16.10
intermediate early
protein ZK637.14 [R
RING-H2 finger pro

A:Cross-references: SGD:S0005493
A:Map position: 15L
A:Note: YOL133w
C:Superfamily: yeast hypothetical protein YOL133w; RING finger homology

Query Match 62.5%; Score 385; DB 2; Length 121;
Best Local Similarity 56.6%; Pred. No. 5.3e-34;
Matches 64; Conservative 10; Mismatches 29; Indels 10; Gaps 1;
QY 5 MDVDTPSGTSAG-----KKRFVKKNNAVALWAWDIVVDNCAICRNHIMDLICI 54
DB 8 MDVDESONIAQSSNQAPVETKKRFEIKKWTAVAFMSWDIAVDNCAICRNHIMEPCI 67

QY 55 EQQANQASATSECTVANGVCHAFHFCISRWLKTRQVCPDLNREWFQKVG 107
DB 68 ECQPKAMTDTNECAVAGVGNHAFHLCINIKWIKTRDACPDLNQWOLARCG 120

RESULT 7
T18513
hypothetical protein C0845c - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18513

R:Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997

A:Reference number: Z18935
A:Accession: T18513
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-166 <LAW>
A:Cross-references: UNIPROT:O77367; EMBL:Z98551; PIDN:CAB11123.2

C:Genetics:
A:Map position: 3
A:Introns: 19/1
A:Note: C0845c

Query Match 61.4%; Score 378; DB 2; Length 166;
Best Local Similarity 69.6%; Pred. No. 4e-33;
Matches 64; Conservative 5; Mismatches 15; Indels 8; Gaps 1;
QY 22 FEVKKNAVALWAWDIVVDNCAICRNHIMDLICIEQA-----NQASATSECTVANG 73
DB 72 FKTHKSAVAAWSWDISVDNCAICRNHIMDLICIEQAQKTDHENDKDKKIDKEGCTVANG 131

QY 74 VCNHAFHFCISRWLKTRQVCPDLNREWFQK 105
DB 132 VCNHAFHLCISRWLKTRQVCPDLNREWFQK 163

RESULT 8
T29620
hypothetical protein R10A10.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T29620
R:Wamsley, P.; Bradshaw, H.
submitted to the EMBL Data Library, November 1996
A:Description: The sequence of C. elegans cosmid R10A10.
A:Reference number: Z20653

A:Accession: T29620
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-112 <WAM>

A:Cross-references: UNIPROT:P91404; EMBL:U80449; PIDN:AAB37826.1; GSPDB:GN00019; CESP:R10A10
A:Experimental source: strain Bristol N2; clone R10A10

C:Genetics:
A:Gene: CESP:R10A10.2
A:Map position: 1
A:Introns: 17/2; 59/1

C:Superfamily: yeast hypothetical protein YOL133w; RING finger homology

Query Match 43.2%; Score 266; DB 2; Length 112;

Best Local Similarity 41.3%; Pred. No. 2.5e-21;
Matches 45; Conservative 20; Mismatches 32; Indels 12; Gaps 2;

QY 1 MAAAMDVDTPSGTSAGKKR-----FEVKKNAVALWAWDIVVDNCAICRNHIMDL 52
DB 1 MNSSNADSQEGSTSAQKQTANPSESPPFVLKKNALAVWAWDECDTCAICRVHLMEE 60

QY 53 CIEQANQASATSECTVANGVCHAFHFCISRWLKTRQVCPDLNREW 101
DB 61 CLRCQ-----SPPSAECYVWVGDCNHSFHHCCMTQIRQNNRCPCLQKDW 105

RESULT 9

T38652
hypothetical protein SPAC343.03 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T38652

R:Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, August 1997

A:Reference number: Z21804
A:Accession: T38652
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:Residues: 1-94 <MUR>
A:Cross-references: UNIPROT:Q9UT86; EMBL:AL109739; PIDN:CAB52266.1; GSPDB:C

A:Experimental source: strain 972h; cosmid c343
C:Genetics:
A:Gene: SPDB:SPAC343.03

A:Map position: 1
A:Introns: 7/1; 48/1

Query Match 26.7%; Score 164.5; DB 2; Length 94;
Best Local Similarity 33.7%; Pred. No. 1.5e-10;
Matches 28; Conservative 16; Mismatches 30; Indels 9; Gaps 3;

QY 21 RFEVKKNAVALWAWDIVVDN-CAICRNHIMDLICIEQANQASATSECTVANGVCHAF 79
DB 2 KVKILRYHAIANTWTDPKDDVCGICRVFPDFGCCPQC-----TSPGDNCPVWGCKRHP 56

QY 80 HFHCISRWLKT---RQVCPDLNR 99
DB 57 HAHCIQWLATSGSQGQCPMDRQ 79

RESULT 10

T21802
hypothetical protein F35G12.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21802

R:Chui, C.
submitted to the EMBL Data Library, October 1994

A:Reference number: Z19473
A:Accession: T21802

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-135 <WIL>

A:Cross-references: UNIPROT:Q20052; EMBL:Z46242; PIDN:CAA86328.1; GSPDB:GN00021; CESP:F35G12
A:Experimental source: clone F35G12

C:Genetics:
A:Gene: CESP:F35G12.9
A:Map position: 3
A:Introns: 33/3; 57/3

C:Superfamily: yeast hypothetical protein YOL133w; RING finger homology
F:68-133/Domain: RING finger homology <RRN>

Query Match 23.8%; Score 146.5; DB 2; Length 135;

Best Local Similarity 33.3%; Pred. No. 1.8e-08;
Matches 28; Conservative 10; Mismatches 35; Indels 11; Gaps 3;

QY 24 VKKNNAVALWAW-DIVVDNCAICRNHIMDLICIEQANQASATSECTVANGVCHAFPH 82

Db 53 VKKLHVCGEWMKQGGEDTCGICRMFEFSAC-----NMCKFPFGDDCPLVLGICRHAFHRH 107

QY 83 CLSRWL-----KTRQVCLDNREW 101

Db 108 CIDKWIAPTNPQFRAQCPLCRQDW 131

RESULT 11

S52511

hypothetical protein YDL008w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein D2900

C:Species: Saccharomyces cerevisiae

C>Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C:Accession: S52511; S67540

R:Andre, B.; Viissers, S.; Urrestarazu, L.

submitted to the EMBL Data Library, February 1995

A:Description: The sequence of a 42 kb segment located on the left arm of chromosome IV

A:Reference number: S52492

A:Accession: S52511

A:Molecule type: DNA

A:Residues: 1-165 <AND>

A:Cross-references: UNIPROT:Q12157; EMBL:Z48432; NID:G683669; PIDN:CAA88351.1; PID:G68366

A:Experimental source: strain S288C

R:Urrestarazu, L.A.; Andre, B.; Viissers, S.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67535

A:Accession: S67540

A:Molecule type: DNA

A:Residues: 1-165 <URR>

A:Cross-references: EMBL:Z74056; NID:G1430968; PIDN:CAA98564.1; PID:e252972; PID:G143096

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:APC11

A:Cross-references: SGB:S0002166

A:Map position: 4L

Query Match 22.1%; Score 136; DB 2; Length 165;

Best Local Similarity 26.4%; Pred. No. 2.8e-07;

Matches 28; Conservative 19; Mismatches 33; Indels 26; Gaps 3;

QY 21 RFEVKKNVALWAWDIV-----VDNCAICRNHIMDLCTEQANQAS 62

Db 2 KVKINEVHSFVAMSHIPSTSDAANDPIGNDEDEVCGICRASVGTCPSCK----- 56

QY 63 ATSEECTVANGVCNHAHFHCISRWLKT---RQVCLDNREWEFOK 105

Db 57 FPGDQCPLVTGLCHHNFHDHCHYRWLDTPTSKGLCPWCRTQFLQK 102

RESULT 12

G90113

Rbpl protein [imported] - Guillardia theta nucleomorph

C:Species: nucleomorph Guillardia theta

A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C:Accession: G90113

R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reid

Nature 410, 1091-1096, 2001

A:Title: The highly reduced genome of an enslaved algal nucleus.

A:Reference number: A99082; MUID:I1323671; PMID:I1323671

A:Accession: G90113

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-99 <DOU>

A:Cross-references: UNIPROT:Q9AVZ5; GB:AJ010592; NID:G12580758; PIDN:CAC27076.1; GSPDB:G

C:Genetics:

A:Map position: 2

A:Genome: nucleomorph

C:Keywords: nucleomorph

Query Match 21.5%; Score 132.5; DB 2; Length 99;

Best Local Similarity 33.3%; Pred. No. 4e-07;

Matches 24; Conservative 14; Mismatches 27; Indels 7; Gaps 1;

QY 40 DNCAICRNHIMDLCTEQ-----ANQASATSEECTVANGVCNHAHFHCISRWLKTRQ 92

Db 22 EKCAICRNLEDNADPFERVGKSKNFLDQISKNCFLAYGRCGHSFHLICIENWILNK 81

QY 93 VCPLDNREWEFOK 104

Db 82 NCPLCSRIWVYE 93

RESULT 13

T20241

hypothetical protein H05L14.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T20241; T23049

R:Wilkinson, J.

submitted to the EMBL Data Library, June 1996

A:Reference number: Z19241

A:Accession: T20241

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-2160 <WIL>

A:Cross-references: UNIPROT:O17709; EMBL:Z75533; PIDN:CAA99823.1; GSPDB:GN00019; CESP:H0:

A:Experimental source: clone C54G4

R:Barlow, K.

submitted to the EMBL Data Library, October 1997

A:Reference number: Z19662

A:Accession: T23049

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-2160 <WIL>

A:Cross-references: EMBL:Z99772; PIDN:CAB16922.1; GSPDB:GN00019; CESP:H05L14.2

A:Experimental source: clone H05L14

C:Genetics:

A:Gene: CESP:H05L14.2

A:Map position: 1

A:Introns: 49/3; 130/3; 190/3; 237/3; 290/1; 463/3; 507/1; 524/2; 545/1; 636/2; 663/2; 7/2; 7/2;

Query Match 18.9%; Score 116.5; DB 2; Length 2160;

Best Local Similarity 30.5%; Pred. No. 0.00044;

Matches 29; Conservative 11; Mismatches 38; Indels 17; Gaps 3;

QY 8 DTPSGTNGAGKRFVKKNVALWAWDIV---DNCAICRNHIMDLCTEQANQASAT 64

Db 2068 DVPMPFSETVMKKMFQCSGYELDVVTEREEVVEEDGCLIC-TEITEAVE----- 2117

QY 65 SEECTVANGVCNHAHFHCISRWLKTRQVCLDNR 99

Db 2118 ----TVTCDTCTREYVHCISRWLKINSVCPQCSR 2148

RESULT 14

T06680

hypothetical protein T17F15.100 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T06680

R:Queirer, F.; Choiane, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigue

submitted to the Protein Sequence Database, April 1999

A:Reference number: Z15793

A:Accession: T06680

A:Molecule type: DNA

A:Residues: 1-349 <QUE>

A:Cross-references: UNIPROT:Q9SU66; EMBL:AL049658; GSPDB:GN00061; ATSP:T17F15.100

A:Experimental source: cultivar Columbia; BAC clone T17F15

C:Genetics:

A:Gene: ATSP:T17F15.100

A:Map position: 3

A:Introns: 26/1; 81/2

F:203-254/Domain: RING finger homology <RRN>

Query Match

16.9%; Score 104; DB 2; Length 349;

```

Query Match      16.6%; Score 102.5; DB 2; Length 249;
Best Local Similarity 26.0%; Pred. No. 0.0016;
Matches 27; Conservative 22; Mismatches 38; Indels 17; Gaps 4;

Qy      5 MDVDTPTSGTNSGAGKKRFEVKKNAVALM-----AWDIVDNCALCRNHI-----MDL 52
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Ddb     125 IDMAITSSSSSRGRGWBEIKWIKTEFYKANKAAENLLID--SYCYNVLNVATTEENG 182

Qy      53 CIECQANQASATSEECTVAGVNCVNHAFPHFCHISRWLKTRQVCPL 96
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Ddb     183 CAICNEDYIEGSS---IVAKLPCDHEFHGDCINKVQLQLNHMGCP 223
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Search completed: June 23, 2005, 15:30:28
Job time : 40 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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Best Available Copy

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2005, 15:18:51 ; Search time 176 Seconds
(without alignments)
314.230 Million cell updates/sec

Title: US-09-541-462B-2

Perfect score: 616

Sequence: 1 MAAMDVTPSGTNSGAGKK.....KTRQVCLDNREWFQKYGH 108

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	616	100.0	1 RBX1_HUMAN	P62877 homo sapien
2	616	100.0	1 RBX1_MOUSE	P62878 mus musculus
3	616	100.0	2 Q641T4	Q641t4 xenopus lae
4	605	98.2	111 2 Q642J6	Q642j6 brachydanio
5	604	98.1	108 1 RBX1_SALSA	Q8G664 salmo salar
6	539.5	87.6	174 2 Q7Q9J7	Q7Q9j7 anopheles g
7	534	86.7	108 1 RBXA_DROME	Q9W561 drosophila
8	523.5	85.0	114 2 Q8S3S0	Q8S3s0 oryza sativ
9	523.5	85.0	123 2 Q657Y3	Q657y3 oryza sativ
10	523	84.9	110 2 Q7Y042	Q7Y042 populus tom
11	514.5	83.5	118 1 RBXA_ARATH	Q940x7 arabidopsis
12	505	82.0	116 2 Q7SE71	Q7se71 neurospora
13	499	81.0	115 1 RBXB_ARATH	Q9M2B0 arabidopsis
14	493	80.0	110 1 RBX1_CABEL	Q23457 caenorhabdi
15	469	76.1	107 1 RBX1_SCHPO	O13959 schizosacch
16	400.5	65.0	122 1 RBXB_DROME	Q9Nhx0 drosophila
17	400	64.9	115 2 Q6BKZ3	Q6bkz3 debaryomyce
18	399	64.8	186 2 Q6CE99	Q6ce99 yarrowia li
19	385	62.5	121 1 RBX1_YEAST	Q8CE273 saccharomyc
20	384	62.3	108 2 Q7SAV1	Q7sav1 ashbya gos
21	383	62.2	107 2 Q7RQX0	Q7rqx0 plasmodium
22	378	61.4	107 2 Q77367	Q77367 plasmodium
23	348.5	56.6	110 2 Q6CP68	Q6cp68 kluyveromyc
24	308	50.0	92 2 Q8SWJ6	Q8swj6 encephalito
25	292	47.4	113 1 RBX2_HUMAN	Q9wtz1 mus musculu
26	290.5	47.2	113 1 RBX2_MOUSE	Q9wtz1 mus musculu
27	284.5	46.2	113 2 Q7PV67	Q7pv67 drosophila
28	284	46.1	109 2 Q7PNW0	Q7pnw0 anopheles g
29	281.5	45.7	96 2 Q6NU82	Q6nu82 xenopus lae
30	266	43.2	112 2 P91404	P91404 caenorhabdi
31	210	34.1	84 2 Q940X6	Q940x6 arabidopsis

32	209	33.9	84	1	AN11_MOUSE	Q9CPX9 mus musculu
33	208	33.8	84	1	AN11_HUMAN	Q9NYG5 homo sapien
34	202.5	32.9	91	2	Q7Q443	Q7q443 anopheles g
35	198	32.1	84	2	Q8H306	Q8h306 oryza sativ
36	197	32.0	85	2	Q7KA43	Q7ka43 drosophila
37	179	29.1	89	2	Q7QX96	Q7qx96 giardia lam
38	169.5	27.5	109	2	Q6C1E3	Q6c1e3 yarrowia li
39	164.5	26.7	94	1	Y1P3_SCHPO	Q9ut86 schizosacch
40	154	25.0	86	2	Q7RGA3	Q7rga3 plasmodium
41	151	24.5	89	2	Q6LFF9	Q6lff9 plasmodium
42	147	23.9	162	2	Q6CMU0	Q6cmu0 kluyveromyc
43	146.5	23.8	135	2	Q20052	Q20052 caenorhabdi
44	141	22.9	57	2	Q9M9L0	Q9m9l0 arabidopsis
45	140	22.7	149	2	Q6FQP6	Q6fqp6 candida gla

ALIGNMENTS

RESULT 1

RBX1_HUMAN

ID RBX1_HUMAN STANDARD; PRT; 108 AA.

AC P62877; Q8N628; Q9DLS2; Q9WUK9; Q9Y254;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE RING-box protein 1 (Rbx1) (Regulator of cullins 1) (RING finger protein 75) (ZYP protein).

GN Name=RBX1; Synonyms=RNF75, ROC1;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A., INTERACTION WITH CULLINS, AND MUTAGENESIS OF CYS-53; CYS-56; CYS-75 AND HIS-77.

RC TISSUE=Cervical carcinoma;

RX MEDLINE=99247022; PubMed=10230407; DOI=10.1016/S1097-2765(00)80482-7; Ohta T., Michel J.J., Schottelius A.J., Xiong Y.; "ROC1, a homolog of Apc11, represents a family of cullin partners with an associated ubiquitin ligase activity."; Mol. Cell 3:535-541(1999).

RL [2]

RN SEQUENCE FROM N.A., AND IDENTIFICATION IN CBC(VHL) COMPLEX. MEDLINE=99234320; PubMed=10213691; DOI=10.1126/science.284.5414.657; Kamura T., Koeppe D.M., Conrad M.N., Skowyra D., Moreland R.J., Iliopoulos O., Lane W.S., Kaelin W.G. Jr., Elledge S.J., Conaway R.C., Harper J.W., Conaway J.W.; "Rbx1, a component of the VHL tumor suppressor complex and SCF ubiquitin ligase."; Science 284:657-661(1999).

RL [3]

RN SEQUENCE FROM N.A.

RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A., Cole C.G., Goward M.E., Aguado B., Mallia M., Mokrab Y., Huckle E.J., Beare D.M., Dunham I.; "A genome annotation driven approach to cloning the human ORFeome."; Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.

RL [4]

RN SEQUENCE FROM N.A.

RP MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031; Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M., Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babage A.K., Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J., Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E., Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Evans K.L., Fey J.M., Fleming K., French L., Garner A.A., Gilbert J.G.R., Goward M.E., Grahm D.V., Griffiths M.N.D., Hall C., Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,

- RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
 RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
 RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
 RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
 RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,
 RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
 RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
 RA Vaudin M., Walli M., Wallis J.M., Whiteley M.N., Willey D.L.,
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S.,
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
 RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
 RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
 RA Fulton R., Johnson D., Benis G., Bentley D., Bradshaw H., Bourne S.,
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
 RA Schect P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
 RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
 RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
 RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
 RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
 RA Peyrard M., Kedra D., Serousi B., Franses I., Tapia I., Bruder C.E.,
 RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
 RA Khan A.S., Lane L., Tiliahun Y., Wright H.,
 RA "The DNA sequence of human chromosome 22.",
 RL Nature 402:489-495(1999).
 [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=brain, and Placenta;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Kzywinski M.I., Skaleka U., Smalus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [6]
 RP SEQUENCE OF 14-108 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20106778; PubMed=10643962;
 RA Perin J.-P., Seddighi N., Charbonnier F., Goudou D., Belkadi L.,
 RA Rieger F., Alliel P.M.,
 RA "Genomic organization and expression of the ubiquitin-proteasome
 RT complex-associated protein Rbx1/ROC1/Hrt1.",
 RL Cell. Mol. Biol. 45:1131-1137(1999).
 [7]
 RN SEQUENCE OF 92-105, INTERACTION WITH CUL1, AND IDENTIFICATION IN A
 RP COMPLEX WITH CUL1, SKP1 AND SKP2.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=99247021; PubMed=10230406; DOI=10.1016/S1097-2765(00)80481-5;
 RA Tan P., Fuchs S.-Y., Chen A., Wu K., Gomez C., Ronai Z., Pan Z.-Q.,
 RT "Recruitment of a ROC1-CUL1 ubiquitin ligase by Skp1 and HOS to
 RL catalyze the ubiquitination of I kappa B alpha.",
 RL Mol. Cell 3:527-533(1999).
 [8]
 RN FUNCTION.
 RP MEDLINE=20047893; PubMed=10579999; DOI=10.1101/gad.13.22.2928;
 RA Kamura T., Conrad M.N., Yan Q., Conaway R.C., Conaway J.W.,
 RT "The Rbx1 subunit of SCF and VHL E3 ubiquitin ligase activates Rbx1
 RT modification of cullins Cdc53 and Cul2.",
 RL Genes Dev. 13:2928-2933(1999).
 [9]
 RN FUNCTION, AND SUBCELLULAR LOCATION.
 RP MEDLINE=20481777; PubMed=11027288;
 RX DOI=10.1126/MCB.20.21.8185-8197.2000;
 RA Furukawa M., Zhang Y., McCarville J., Ohta T., Xiong Y.,
 RT "The CUL1 C-terminal sequence and ROC1 are required for efficient
 RT nuclear accumulation, NEDD8 modification, and ubiquitin ligase
 RT activity of CUL1.",
 RL Mol. Cell. Biol. 20:8185-8197(2000).
 [10]
 RN IDENTIFICATION IN E3 UBIQUITIN LIGASE COMPLEX WITH MUF1, AND
 RP IDENTIFICATION IN COMPLEXES WITH CUL5.
 RX MEDLINE=21380117; PubMed=11384984; DOI=10.1074/jbc.M103093200;
 RA Kamura T., Burian D., Yan Q., Schmidt S.L., Lane W.S., Querido E.,
 RA Branton P.E., Shlatifard A., Conaway R.C., Conaway J.W.,
 RT "Muf1, a novel elongin BC-interacting leucine-rich repeat protein that
 RT can assemble with Cul5 and Rbx1 to reconstitute a ubiquitin ligase.",
 RL J. Biol. Chem. 276:29748-29753(2001).
 [11]
 RN IDENTIFICATION IN E3 UBIQUITIN LIGASE COMPLEX WITH MED8.
 RX MEDLINE=22155962; PubMed=12149480; DOI=10.1073/pnas.162424199;
 RA Brower C.S., Sato S., Tomomori-Sato C., Kamura T., Pause A.,
 RA Stearman R., Klausner R.D., Malik S., Lane W.S., Sorokina I.,
 RA Roeder R.G., Conaway J.W., Conaway R.C.,
 RT "Mammalian mediator subunit mMED8 is an elongin BC-interacting protein
 RT that can assemble with Cul2 and Rbx1 to reconstitute a ubiquitin
 RT ligase.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:10353-10358(2002).
 [12]
 RN IDENTIFICATION IN SCF-LIKE COMPLEX, AND INTERACTION WITH CUL7.
 RX MEDLINE=22388271; PubMed=12481031; DOI=10.1073/pnas.252646399;
 RA Dias D.C., Dolios G., Wang R., Pan Z.O.,
 RT "CUL7: a DCC domain-containing cullin selectively binds Skp1.Fbx29 to
 RT form an SCF-like complex.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16601-16606(2002).
 [13]
 RN X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 19-108 IN COMPLEX WITH 17-776
 RP OF CUL1, AND X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) IN SCF COMPLEX WITH
 RP CUL1, SKP1 AND SKP2.
 RX MEDLINE=2159435; PubMed=11961546; DOI=10.1038/416703a;
 RA Zheng N., Schulman B.A., Song L., Miller J.J., Jeffrey P.D., Wang P.,
 RA Chu C., Kopp D.M., Elledge S.J., Pagano M., Conaway R.C.,
 RA Conaway J.W., Harper J.W., Pavletich N.P.,
 RT "Structure of the Cull1-Rbx1-Skp1-F boxSkp2 SCF ubiquitin ligase
 RT complex.",
 RL Nature 416:703-709(2002).
 CC -1- FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) and the
 CC CBC(VHL) (CUL2-elongin BC-VHL) E3 ubiquitin ligase complexes,
 CC which mediate the ubiquitination and subsequent proteasomal
 CC degradation of target proteins involved in cell cycle progression,
 CC signal transduction and transcription. Through the RING-type zinc
 CC finger, seems to recruit the E2 ubiquitination enzyme, like CDC34,
 CC to the complex and brings it into close proximity to the
 CC substrate. Probably also stimulates CDC34 autoubiquitination.
 CC Promotes the neddylation of CUL1 and probably CUL2.
 CC -1- PATHWAY: Ubiquitin conjugation; third step.
 CC -1- SUBUNIT: Part of a SCF complex consisting of CUL1, Rbx1, Skp1 and
 CC SKP2. Part of a SCF-like complex consisting of CUL1, Rbx1, Skp1
 CC and FBXW8. Part of CBC(VHL) complexes with elongin BC complex
 CC (TCEB1 and TCEB2), CUL2 or CUL5 and VHL. Part of multisubunit E3
 CC ubiquitin ligase complexes with elongin BC complex (TCEB1 and
 CC TCEB2), CUL2 and MED8; elongin BC complex (TCEB1 and TCEB2), CUL5
 CC and MUF1. Part of multisubunit complexes with elongin BC complex
 CC (TCEB1 and TCEB2), elongin A/TCEB3 or SOCS1 or WSB1 and CUL5.
 CC Interacts directly with CUL1 and probably also with CUL2, CUL3,
 CC CUL4A, CUL4B, CUL5 and CUL7. Probably interacts with CDC34.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC -!- TISSUE SPECIFICITY: Widely expressed.

Query Match 100.0%; Score 616; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 6.6e-61;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAAMDVTPSTNSGAGKREVEKNAVALAWNDVVDNCAICRNHIMDLICISQANQ 60
DB 1 MAAAMDVTPSTNSGAGKREVEKNAVALAWNDVVDNCAICRNHIMDLICISQANQ 60

QY 61 ASATSEECTVANGVNCNHFPHFHCISRWLKTRQVCPDLNREWEFKYGH 108
DB 61 ASATSEECTVANGVNCNHFPHFHCISRWLKTRQVCPDLNREWEFKYGH 108

RESULT 2
RBX1 MOUSE
ID RBX1 MOUSE STANDARD; PRT: 108 AA.
AC P62878; Q8N628; Q9D1S2; Q9WUK9; Q9Y2S4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE RING-box protein 1 (Rbx1).
GN Name=Rbx1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND IDENTIFICATION IN CBC(VHL) COMPLEX.
RX MEDLINE=99234320; PubMed=10213691; DOI=10.1126/science.284.5414.657;
RA Kamura T., Koepf D.M., Conrad M.N., Skowra D., Moreland R.J.,
RA Iliopoulos O., Lane W.S., Kaelin W.G. Jr., Ellledge S.J., Conway R.C.,
RA Harper J.W., Conway J.W.;
RT "Rbx1, a component of the VHL tumor suppressor complex and SCF
RT ubiquitin ligase.";
RL Science 284:657-661(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=23354683; PubMed=12477932; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamana H., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gofjorbi T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Bruscia V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovskiy N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reid D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wegner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura N., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [3]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain, and Breast tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP IDENTIFICATION IN E3 UBIQUITIN LIGASE COMPLEX WITH MUF1, AND
RP IDENTIFICATION IN COMPLEXES WITH CUL5.
RX MEDLINE=21380117; PubMed=11384984; DOI=10.1074/jbc.M103093200;
RA Kamura T., Burian D., Yan Q., Schmidt S.L., Lane W.S., Querido E.,
RA Branton P.E., Shilatifard A., Conway R.C., Conway J.W.;
RT "Muf1, a novel Elongin BC-interacting leucine-rich repeat protein that
RT can assemble with Cul5 and Rbx1 to reconstitute a ubiquitin ligase.";
RL J. Biol. Chem. 276:29748-29753(2001).
RN [5]
RP TISSUE SPECIFICITY.
RX MEDLINE=20106778; PubMed=10643962;
RA Perin J.-P., Seddigi N., Charbonnier F., Goudou D., Belkadi L.,
RA Rieger F., Alliel P.M.;
RT "Genomic organization and expression of the ubiquitin-proteasome
RT complex-associated protein Rbx1/ROCI/Hrt1.";
RL Cell. Mol. Biol. 45:1131-1137(1999).
CC -!- FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) and the
CC CBC(VHL) (CUL2-elongin BC-VHL) E3 ubiquitin ligase complexes,
CC which mediate the ubiquitination and subsequent proteasomal
CC degradation of target proteins involved in cell cycle progression,
CC signal transduction and transcription. Through the RING-type zinc
CC finger, seems to recruit the E2 ubiquitination enzyme, like CDC34,
CC to the complex and brings it into close proximity to the
CC substrate. Probably also stimulates CDC34 autoubiquitination.
CC Promotes the neddylation of CUL1 and probably CUL2 (By
CC similarity).
CC -!- PATHWAY: Ubiquitin conjugation; third step.
CC -!- SUBUNIT: Part of a SCF complex consisting of CUL1, Rbx1, SKP1 and
CC SKP2. Part of a SCF-like complex consisting of CUL7, Rbx1, SKP1
CC (TCEB1 and TCEB2), CUL2 or CUL5 and VHL. Part of multisubunit E3
CC ubiquitin ligase complexes with elongin BC complex (TCEB1 and
CC TCEB2), CUL2 and MED8; elongin BC complex (TCEB1 and TCEB2), CUL5
CC and MUF1. Part of multisubunit complexes with elongin BC complex
CC (TCEB1 and TCEB2), elongin A/TCEB3 or SOCS1 or WSB1 and CUL5.
CC Interacts directly with CUL1 and probably also with CUL2, CUL3,
CC CUL4A, CUL4B, CUL5 and CUL7. Probably interacts with CDC34.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -!- TISSUE SPECIFICITY: Widely expressed.
CC -!- DOMAIN: The RING-type zinc finger domain is essential for
CC ubiquitin ligase activity. It coordinates an additional third zinc
CC atom.
CC -!- SIMILARITY: Belongs to the RING-box family.
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC
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CC -----
CC EMBL; AF140599; AAD29716.1; -.
CC EMBL; AK003159; BAB22612.1; -.
CC EMBL; BC027396; -, NOT_ANNOTATED_CDS.
CC EMBL; BC056992; AAH56992.1; -.
CC DR MGD; MGI:1891829; Rbxi.
CC DR InterPro; IPR001841; Znf_ring.
CC DR Pfam; PF00097; zf-C3HC4_1.
CC DR PROSITE; PS00089; ZF_RING_2; 1.
CC KW Metal-binding; Nuclear protein; Ubl conjugation pathway; Zinc;
KW Zinc-finger.
FT ZN FING 53 98 RING-type.
FT METAL 42 42 Zinc 1 (By similarity).
FT METAL 45 45 Zinc 1 (By similarity).
FT METAL 53 53 Zinc 3 (By similarity).
FT METAL 56 56 Zinc 3 (By similarity).
FT METAL 68 68 Zinc 3 (By similarity).
FT METAL 75 75 Zinc 2 (By similarity).
FT METAL 77 77 Zinc 2 (By similarity).
FT METAL 80 80 Zinc 1 (By similarity).
FT METAL 82 82 Zinc 3 (By similarity).
FT METAL 83 83 Zinc 1 (By similarity).
FT METAL 94 94 Zinc 2 (By similarity).
FT METAL 97 97 Zinc 2 (By similarity).
FT CONFLICT 42 42 C -> F (in ref. 2).
SQ SEQUENCE 108 AA; 12274 MW; 30FC5ADF66096C0E CRC64;

Query Match 100.0%; Score 616; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 6.6e-61;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAAMDVDTPTSGTNSGAGKKRFVKKNNAVALWAWDIVVDNCAICRNHIMDLICIECQAO 60
DB 1 MAAAMDVDTPTSGTNSGAGKKRFVKKNNAVALWAWDIVVDNCAICRNHIMDLICIECQAO 60

QY 61 ASATSECTVAVGVCNHAHFHHCISRWLKTRQVCPLDNRWEFQKYGH 108
DB 61 ASATSECTVAVGVCNHAHFHHCISRWLKTRQVCPLDNRWEFQKYGH 108

RESULT 3
Q641T4 PRELIMINARY; PRT; 108 AA.
AC Q641T4 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RA Klein S., Gerhard D.S.;
RA EMBL; BC082183; AAH82183.1; -.
KW Hypothetical protein.
SQ SEQUENCE 108 AA; 12274 MW; 30FC5ADF66096C0E CRC64;

Query Match 100.0%; Score 616; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 6.6e-61;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAAMDVDTPTSGTNSGAGKKRFVKKNNAVALWAWDIVVDNCAICRNHIMDLICIECQAO 60
DB 1 MAAAMDVDTPTSGTNSGAGKKRFVKKNNAVALWAWDIVVDNCAICRNHIMDLICIECQAO 60

QY 61 ASATSECTVAVGVCNHAHFHHCISRWLKTRQVCPLDNRWEFQKYGH 108
DB 61 ASATSECTVAVGVCNHAHFHHCISRWLKTRQVCPLDNRWEFQKYGH 108

RESULT 4
Q642J6 PRELIMINARY; PRT; 111 AA.
AC Q642J6
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein (Fragment).
OS Brachydanio rerio (Zebrafish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=liver;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
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CC 5 MDVD-----TPSGTSGAGKRPVKWNAVALWANDI VDNCAI CRNHINDLCTEQAN 59

Db	66	MDIDEEFEAPTSSSSRGRGRKFEVKKMNAVALAWDIIVDNCALCRNHIMDLCTECQAN	125	RT	"Annotation of the Drosophila melanogaster euchromatic genome: a systematic review."
Qy	60	QASATSEECTVAGVNCNHFHCHCISRWLTKRQVCPDLNREWEFOKYGH	108	RL	Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
Db	126	QASATSEECTVAGVNCNHFHCHCISRWLTKRQVCPDLNREWEFOKYGH	174	RN	[3]
Db	126	QASATSEECTVAGVNCNHFHCHCISRWLTKRQVCPDLNREWEFOKYGH	174	RP	SEQUENCE FROM N.A.
RESULT 7				RC	STRAIN=Oregon-R;
REXA_DROME				RX	MEDLINE=20196011; PubMed=10731137; DOI=10.1126/science.287.5461.2220;
AC	Q9W5E1; 077429;	STANDARD;	PRT; 108 AA.	RA	Bencos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
DT	10-OCT-2003 (Rel. 42, Created)			RA	Bartell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
DT	10-OCT-2003 (Rel. 42, Last sequence update)			RA	Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
DE	25-JAN-2005 (Rel. 46, Last annotation update)			RA	Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
DE	RING-box protein 1A (Regulator of cullins 1a) (dbx1).			RA	Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablo B.,
GN	Name=Rocla; ORFNames=CG16982;			RA	Modelle J., Peter A., Schoettler P., Werner M., Mourikoti F.,
OS	Drosophila melanogaster (fruit fly).			RA	Beirnt N., Dowe G., Schaefer U., Jaekle H., Bucheton A.,
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			RA	Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			RA	McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
OC	Ephydroidea; Drosophilidae; Drosophila.			RA	Glover D.M.;
OX	NCBI_TaxID=7227;			RT	"From sequence to chromosome: the tip of the X chromosome of D.
RN	[1]			RL	melanogaster.";
RP	SEQUENCE FROM N.A.			RL	Science 287:2220-2222(2000).
RC	STRAIN=Berkely;			RN	[4]
RX	MEDLINE=20196006; PubMed=12537569;			RP	SEQUENCE FROM N.A.
RA	Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,			RC	STRAIN=Berkely; TISSUE=Embryo;
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,			RX	MEDLINE=22426066; PubMed=12537569;
RA	George R.A., Lewis S.B., Richards J.R., Vande M.D., Zhang Q., Chen L.X.,			RA	Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA	Sutton G.G., Wortman J.R., Vande M.D., Zhang Q., Chen L.X.,			RA	George R.A., Guarin H., Krommiller B., Pacleb J.M., Park S., Wan K.H.,
RA	Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,			RA	Rubin G.M., Celnik S.E.;
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Baldwin D.G.,			RT	"A Drosophila full-length cDNA resource.";
RA	Abriel J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.G.,			RL	[5]
RA	Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,			RP	FUNCTION, TISSUE SPECIFICITY, DEVELOPMENTAL STAGE, AND MUTAGENESIS OF
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,			RP	ASN-59 AND CYS-68.
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,			RX	MEDLINE=22057626; PubMed=12062088; DOI=10.1016/S1534-5807(02)00164-8;
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,			RA	Noureddine M.A., Donaldson T.D., Thacker S.A., Duronio R.J.;
RA	Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,			RT	"Drosophila Rocla encodes a RING-H2 protein with a unique function in
RA	de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,			RT	processing the Hh signal transducer Ci by the SCF E3 ubiquitin
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,			RL	ligase.";
RA	Durbini K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,			RN	[6]
RA	Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,			RP	INTERACTIONS WITH LIN19 AND SLMB.
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,			RX	MEDLINE=21391618; PubMed=11500045; DOI=10.1006/bbrc.2001.5394;
RA	Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,			RA	Bocca S.N., Muzzopappa M., Silberstein S., Wappner P.;
RA	Hoslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,			RT	"Occurrence of a putative SCF ubiquitin ligase complex in
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,			RT	Drosophila.";
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,			RL	Biochem. Biophys. Res. Commun. 286:357-364(2001).
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,			RP	REVIEW ON E3 UBIQUITIN LIGASE COMPLEXES.
RA	Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,			RX	MEDLINE=22736111; PubMed=12850443; DOI=10.1016/S0168-9525(03)00146-X;
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,			RA	Ou C.-Y., Pi H., Chien C.-T.;
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,			RT	"Control of protein degradation by E3 ubiquitin ligases in Drosophila
RA	Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,			RT	eye development.";
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,			RL	Trends Genet. 19:382-389(2003).
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,			CC	-!- FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,			CC	ubiquitin ligase complex, which mediates the ubiquitination and
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,			CC	subsequent proteasomal degradation of target proteins. Through the
RA	Wang Z.-Y., Wasearman D.A., Weinstein G.M., Weissenbach J.,			CC	RING-type zinc finger, seems to recruit the E2 ubiquitination
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,			CC	enzyme to the complex and brings it into close proximity to the
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,			CC	substrate. Required for the specific SCF-dependent proteolysis of
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,			CC	Ci, but not that of ARM, suggesting that it also participates in
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;			CC	the selection of substrates inside the SCF complex.
RT	"The genome sequence of Drosophila melanogaster.";			CC	-!- PATHWAY: Ubiquitin conjugation; third step.
RL	Science 287:2185-2195(2000).			CC	-!- SUBUNIT: Part of a SCF complex consisting of Skp1 (SKP1), Lin19
RN	[2]			CC	(CUL1), Rocla and F-box protein Slmb. Interacts directly with
RP	GENOME REANNOTATION.			CC	Lin19 and Slmb.
RX	MEDLINE=22426069; PubMed=12537572;			CC	-!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
RA	Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,			CC	-!- TISSUE SPECIFICITY: Widely expressed. Expressed in embryonic,
RA	Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,			CC	larval and adult tissues.
RA	Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,			CC	-!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically.
RA	Battencourt B.R., Celnik S.E., de Grey A.D.N.J., Drysdale R.A.,			CC	-!- DOMAIN: The RING-type zinc finger domain is essential for
RA	Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,			CC	ubiquitin ligase activity. It coordinates an additional third zinc
RA	Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,			CC	atom (By similarity).
RA	Lewis S.E.;			CC	-!- SIMILARITY: Belongs to the RING-box family.
				CC	-!- SIMILARITY: Contains 1 RING-type zinc finger.

```
CC -I- CAUTION: Ref.3 sequence differs from that shown due to erroneous
CC gene model prediction.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; AE003418; AAP45536.1; -.
CC DR ENBL; AL031581; CAA20898.1; ALT_SEQ.
CC DR ENBL; AY119265; AAM51125.1; -.
CC DR PIR; T13388; T13388.
CC DR FlyBase; FBgn0025638; Rocla.
CC DR GO; GO:0005634; C:nucleus; IDA.
CC DR GO; GO:0019005; C:SCF ubiquitin ligase complex; IDA.
CC DR GO; GO:0004840; F:ubiquitin conjugating enzyme activity; NAS.
CC DR GO; GO:0008270; F:zinc ion binding; NAS.
CC DR GO; GO:0008283; P:cell proliferation; IMP.
CC DR GO; GO:0007224; P:smoothed receptor signaling pathway; NAS.
CC DR InterPro; IPR001841; Znf_ring.
CC DR Pfam; PF00097; zf-G3HC4_1.
CC DR PROSITE; PS50089; ZF_RING_2; 1.
CC DR Developmental protein; Metal-binding; Nuclear protein;
CC KW Ubl conjugation pathway; Zinc; Zinc-finger.
CC KM ZN_FING 53 98 RING-type.
CC FT DOMAIN 12 15 Poly-Ser.
CC FT METAL 42 42 Zinc 1 (By similarity).
CC FT METAL 45 45 Zinc 1 (By similarity).
CC FT METAL 53 53 Zinc 3 (By similarity).
CC FT METAL 56 56 Zinc 3 (By similarity).
CC FT METAL 68 68 Zinc 3 (By similarity).
CC FT METAL 75 75 Zinc 2 (By similarity).
CC FT METAL 77 77 Zinc 2 (By similarity).
CC FT METAL 80 80 Zinc 1 (By similarity).
CC FT METAL 82 82 Zinc 3 (By similarity).
CC FT METAL 83 83 Zinc 1 (By similarity).
CC FT METAL 94 94 Zinc 2 (By similarity).
CC FT METAL 97 97 Zinc 2 (By similarity).
CC FT MUTAGEN 59 59 N-C: Loss of function; when associated
CC FT with R-68.
CC FT MUTAGEN 68 68 C-R: Loss of function; when associated
CC FT with C-59.
CC SQ SEQUENCE 108 AA; 12538 MW; 15784198281BCD13 CRC64;

Query Match      86.7%; Score 534; DB 1; Length 108;
Best Local Similarity 87.2%; Pred. No. 9.4e-52;
Matches 95; Conservative 4; Mismatches 4; Indels 6; Gaps 2;

Qy   5 MDVD-----TPSGTNSGAGKKRFEVKKNVAVALWANDIVVDNCAICRNHIMDI.CIECOAN 59
    1 :|||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db   1 MEVDEGDYEVPPSSSKG-DKKRFVEVKKNVAVALWANDIVVDNCAICRNHIMDI.CIECOAN 59

Qy   60 QASATSECTVAVGVNCNHAFHFHCISRWLKTRQVCPLDNREWFQKYGH 108
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db   60 QASATSECTVAVGVNCNHAFHFHCISRWLKTRQVCPLDNREWFQKYGH 108

RESULT 8
Q8S380 ID Q8S350 PRELIMINARY; PRT; 114 AA.
AC Q8S350;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative ring box-1 protein [Putative RING box protein 1].
GN Name=49DJ1.12; Synonyms=OSTJB0060016.27-1,
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoidae; Oryzeae; Oryza.
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SQ SEQUENCE 123 AA; 13625 MW; 38260146F7B4DBA7 CRC64;
Query Match 85.0%; Score 523.5; DB 2; Length 123;
Best Local Similarity 77.5%; Pred. No. 1.6e-50;
Matches 93; Conservative 5; Mismatches 5; Indels 17; Gaps 2;

QY 6 DVDTP-----SGTNSGAG-----KKRFEVKKNNAVALWAWDIIVDNCALICRNH 48
DB 4 DINAPPPAPAPAGAGEGSSSAGSPSRKPKRFEIKKNNAVALWAWDIIVDNCALICRNH 63
QY 49 INDLCIECQANQASATSECTVANGVNCNHFHFCISRLWLTQVCPDLNREWEFOKYGH 108
DB 64 INDLCIECQANQASATSECTVANGVNCNHFHFCISRLWLTQVCPDLNREWEFOKYGH 123

RESULT 10
ID QY7042 PRELIMINARY; PRT; 110 AA.
AC QY7042;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ring box protein.
OS Populus tomentosa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
OX NCBI_TaxID=118781;
RN [1]
RP SEQUENCE FROM N.A.
RA Fan J.H.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RC -1- SIMILARITY: Contains 1 RING-type zinc finger.
DR EMBL; AY302066; AAP57304.1; -.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF000097; zfi-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
DR Metal-binding; Zinc; Zinc-finger.
KW SEQUENCE 110 AA; 12591 MW; 0172C6CAE3FA2772 CRC64;
Query Match 84.9%; Score 523; DB 2; Length 110;
Best Local Similarity 84.5%; Pred. No. 1.6e-50;
Matches 93; Conservative 4; Mismatches 7; Indels 6; Gaps 2;

QY 5 MDVD---TPSGACKRFEVKKNNAVALWAWDIIVDNCALICRNHIMDLCECQA 58
DB 1 MDTDTVMVPAGESSSSRRKPKRFEIKKNNAVALWAWDIIVDNCALICRNHIMDLCECQA 60
QY 59 NQASATSECTVANGVNCNHFHFCISRLWLTQVCPDLNREWEFOKYGH 108
DB 61 NQASATSECTVANGVNCNHFHFCISRLWLTQVCPDLNREWEFOKYGH 110

RESULT 11
ID RBXA ARATH STANDARD; PRT; 118 AA.
AC Q94077;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE RING-box protein 1a (RBX1a-At) (At-Rbx1;1) (REX1-2).
GN Name=RBX1A; OrderedLocustNames=At5g20570; ORFNames=F7C8.160;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]

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RP SEQUENCE FROM N.A.
RA Oekresz L.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016721; PubMed=11130714; DOI=10.1038/35048507;
RA Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Kohara M., Matsumoto M., Matsumoto A., Muraki A., Nakayama S.,
RA Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,
RA Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M.,
RA Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M.,
RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,
RA Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strommatt C.,
RA Wagner-McPherson C., Wollam A., Yeakum M., Bell M., Dedhia N.,
RA Parnell L., Shah R., Rodriguez M., Hoon See L., Vil D., Baker J.,
RA Kirchoff K., Toth K., King L., Bahret A., Miller B., Marra M.A.,
RA Martienssen R., McCombie W.R., Wilson R.K., Murphy G., Bancroft I.,
RA Volckaert G., Wambutt R., Duesterhoeft A., Stiekema W., Pohl T.,
RA Lanthan K.-D., Terryn N., Hartley N., Bent E., Johnson S.,
RA Langham S.-A., McCallagh B., Robben J., Grymonprez B., Zimmermann W.,
RA Rampegerger U., Wedler H., Balke K., Wedler E., Peters S.,
RA van Staveren M., Dirkse W., Mooijman P., Klein Lankhorst R.,
RA Weitzenecker T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,
RA Feldpausch M., Lamberth S., Villarroel R., Gielen J., Ardiles W.,
RA Bents O., Lemcke K., Kolesov G., Mayer K.F.X., Rudd S., Schoof H.,
RA Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Franz P.F.;
RT "Sequence and analysis of chromosome 5 of the plant Arabidopsis thaliana.";
RL Nature 408:823-826(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Prover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
RA Feldmann K.;
RT "Full-length cDNA from Arabidopsis thaliana.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;
RA Yamada K., Lim J., Dale J.C., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.-J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newman G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Tang C.C., Onodera C.S., Deng J.M., Lee J.M., Toriumi M.J.,
RA Arakawa T., Barth J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayaashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Ytton S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis genome.";
RL Science 302:842-846(2003).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX PubMed=11910074; DOI=10.1126/science.1071006;
RA Seki M., Narusaka M., Kamiya A., Ishida J., Satou M., Sakurai T.,
RA Nakajima M., Enju A., Akiyama K., Oono Y., Muramatsu M.,
RA Hayaashizaki Y., Kawai J., Carninci P., Itoh M., Ishii Y., Arakawa T.,
RA Shibata K., Shinagawa A., Shinozaki K.;
RT "Functional annotation of a full-length Arabidopsis cDNA collection.";
RN Science 296:141-145(2002).
RN [6]
RP FUNCTION, TISSUE SPECIFICITY, IDENTIFICATION IN A SCF COMPLEX WITH
RP CUL1 AND TIR1, AND INTERACTION WITH CUL1.
RX MEDLINE=22204438; PubMed=12215511;

```

RA Gray W.M., Hellmann H., Dharmasiri S., Estelle M.;
 RT "Role of the Arabidopsis RING-H2 protein RBX1 in RUB modification and
 RL SCF function."; Plant Cell 14:2137-2144(2002).
 RN [7]
 RN FUNCTION, TISSUE SPECIFICITY, IDENTIFICATION IN SCF COMPLEX, AND
 RP INTERACTIONS WITH CUL1; CUL4; ASK1 AND ASK2
 RX MEDLINE=22370998; PubMed=12381738; DOI=10.1074/jbc.M204254200;
 RA Lechner E., Xie D., Grava S., Pigaglio E., Planchais S.,
 RA Murray J.A.H., Parmentier Y., Mutterer J., Dubreucq B., Shen W.-H.,
 RA Genschik P.;
 RT "The AtRbx1 protein is part of plant SCF complexes, and its down-
 RT regulation causes severe growth and developmental defects."; J.
 RL J. Biol. Chem. 277:5069-5080(2002).
 RN [8]
 RN FUNCTION.
 RP MEDLINE=22568282; PubMed=12682009; DOI=10.1093/emboj/cdg190;
 RX Dharmasiri S., Dharmasiri N., Hellmann H., Estelle M.;
 RA "The RUB/Nedd8 conjugation pathway is required for early development
 RT in Arabidopsis."; EMBO J. 22:1762-1770(2003).
 RL [9]
 CC -!- FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3
 CC ubiquitin ligase complex, which mediates the ubiquitination and
 CC subsequent proteosomal degradation of target proteins. The SCF
 CC complex plays a crucial role in regulating response to auxin and
 CC is essential for growth and development. Through the RING-type
 CC zinc finger, seems to recruit the E2 ubiquitination enzyme, to the
 CC complex and brings it into close proximity to the substrate.
 CC Promotes the neddylation of CUL1.
 CC -!- PATHWAY: Ubiquitin conjugation; third step.
 CC -!- SUBUNIT: Part of SCF complexes, which consist of a SKP1-related
 CC protein, a cullin, a RBX protein and a F-box protein. Part of a
 CC SCF complex with ASK1 or ASK2 and CUL1. Part of a SCF complex with
 CC CUL1 and TIR1. Interacts with CUL1 and CUL4.
 CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).
 CC CUL1 and TIR1. Interacts with CUL1 and CUL4.
 CC -!- TISSUE SPECIFICITY: Widely expressed. Expressed in shoot,
 CC silique, meristem, flowers, floral buds, open flowers, leaves,
 CC stems, roots, germinant seeds and seedlings in dark. Expressed at a
 CC higher level in tissues containing actively dividing cells.
 CC -!- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity. It coordinates an additional third zinc
 CC atom.
 CC -!- SIMILARITY: Belongs to the RING-box family.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
 CC
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 CC
 DR EMBL; AF052401; AAL13435.1; -;
 DR EMBL; AF296833; -; NOT_ANNOTATED_CDS.
 DR EMBL; AY086913; AAM64477.1; -;
 DR EMBL; AY072430; AAL62422.1; -;
 DR EMBL; AY114719; AAM48038.1; -;
 DR EMBL; AK118181; BAC42804.1; -;
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Metal-binding; Nuclear protein; Ub1 conjugation pathway; Zinc;
 KW Zinc-finger.
 FT ZN FING 63 108 RING-type.
 FT METAL 52 52 Zinc 1 (By similarity).
 FT METAL 55 55 Zinc 1 (By similarity).
 FT METAL 63 63 Zinc 3 (By similarity).
 FT METAL 66 66 Zinc 3 (By similarity).
 FT METAL 78 78 Zinc 3 (By similarity).
 FT METAL 85 85 Zinc 2 (By similarity).
 FT METAL 87 87 Zinc 2 (By similarity).
 FT METAL 90 90 Zinc 1 (By similarity).

FT METAL 92 92 Zinc 3 (By similarity).
 FT METAL 93 93 Zinc 1 (By similarity).
 FT METAL 104 104 Zinc 2 (By similarity).
 FT METAL 107 107 Zinc 2 (By similarity).
 SQ SEQUENCE 118 AA; 13238 MW; 19947BF06F442A82 CRC64;
 Query Match 83.5%; Score 514.5; DB 1; Length 118;
 Best Local Similarity 78.6%; Pred. No. 1.5e-49;
 Matches 92; Conservative 6; Mismatches 8; Indels 11; Gaps 2;
 QY 3 AAMDVDT---PSG-----TNSGAGKRPVKKNVAVALWAWDIVVDNCAICRNHMD 51
 DB 2 ATLSDVTMTIPAGEASSVVAASSNNKKARFEIKWSAVALWAWDIVVDNCAICRNHMD 61
 QY 52 LCIECQANQASATSECTVAMGVCMHAFHFCISRWLKTQVCPDNDREWEFQKYG 108
 DB 62 LCIECQANQASATSECTVAMGVCMHAFHFCISRWLKTQVCPDNDSEWEFQKYG 118
 RESULT 12
 Q7SBT1 PRELIMINARY; PRT; 116 AA.
 AC Q7SBT1;
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=NGU06224.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OR74A;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Inakiev P., Pedersen D., Nelson M., Washburne M.,
 RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
 RA Kamal M., Kamysseilis M., Maucell E., Bielke C., Rudd S., Frishman D.,
 RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
 RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
 RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
 RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
 RL Nature 0:0-0(2003).
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AABX01000163; EAA33839.1; -;
 DR EMBL; GO:0000151; C:ubiquitin ligase complex; IEA.
 DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0016567; P:protein ubiquitination; IEA.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
 SQ SEQUENCE 116 AA; 13168 MW; BF1D46357C40D802 CRC64;
 Query Match 82.0%; Score 505; DB 2; Length 116;
 Best Local Similarity 94.4%; Pred. No. 1.7e-48;
 Matches 85; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 18 GKPRFEVKKNVAVALWAWDIVVDNCAICRNHMDLCIECQANQASATSECTVAMGVCMH 77
 DB 26 GKPRFEVKKNVAVALWAWDIVVDNCAICRNHMDLCIECQANQASATSECTVAMGVCMH 85

QY 78 AFHFHCISRWLKTQVCPDLNREWEFKYGH 107
 DB 86 AFHFHCISRWLKTQVCPDLNREWEFKYGH 115

RESULT 13
 RBXB ARATH
 ID RBXB ARATH STANDARD; PRT; 115 AA.
 AC Q9X2H0;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Putative RING-box protein 1b (RBX1b-At) (At-Rbx1;2) (RBX1-1).
 GN Name=RBX1b; OrderedLocusNames=At3g42830; ORFNames=T21C14.50;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016720; PubMed=11130713; DOI=10.1038/35048706;
 RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M.,
 RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA Dalseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
 RA De Simone V., Choiane N., Artiguenave F., Robert C., Brottier P.,
 RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simonati B.,
 RA Conrad A., Horischer K., Kauer G., Loehner T., H., Nordsiek G.,
 RA Reichelt J., Scharfe M., Schoen O., Barges M., Terol J., Climent J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
 RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
 RA De Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
 RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walte A., Utterback T., Fujii C.Y., Shea T.P.,
 RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
 RA Pai G., Miltischer J., Sellers P., Gill J.E., Feldblyum T.V.,
 RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 thaliana.";
 RT Nature 408:822-822 (2000).
 RL [2]
 RN DISCUSSION OF SEQUENCE.
 RP MEDLINE=22204438; PubMed=12215511;
 RX Gray W.M., Hellmann H., Dharmasiri S., Estelle M.;
 RA "Role of the Arabidopsis RING-H2 protein RBX1 in RUB modification and
 SCF function.";
 RT Plant Cell 14:2137-2144 (2002).
 RN [3]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=22370998; PubMed=12381738; DOI=10.1074/jbc.M204254200;
 RA Lechner E., Xie D., Grava S., Pigaglio E., Planchais S., Shen W.-H.,
 RA Murray J.A.H., Parmentier Y., Mutterer J., Dubreucq B., Shen W.-H.,
 RA Genschik P.;
 RT "The AtRbx1 protein is part of plant SCF complexes, and its down-
 regulation causes severe growth and developmental defects.";
 RT J. Biol. Chem. 277:50069-50080 (2002).
 RL -1- FUNCTION: Potential component of the SCF (SKP1-CUL1-F-box protein)
 CC E3 ubiquitin ligase complex, which mediates the ubiquitination and
 CC subsequent proteasomal degradation of target proteins. The SCF
 CC complex plays a crucial role in regulating response to auxin and

is essential for growth and development. Through the RING-type
 zinc finger, seems to recruit the E2 ubiquitination enzyme, to the
 complex and brings it into close proximity to the substrate (By
 similarity).
 CC -!- PATHWAY: Ubiquitin conjugation; third step.
 CC -!- SUBUNIT: Potential part of SCF complexes, which consist of a SKP1-
 related protein, a cullin, a RBX protein and a F-box protein.
 CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).
 CC -!- TISSUE SPECIFICITY: Not detected in floral buds, stems and roots.
 CC -!- DOMAIN: The RING-type zinc finger domain is essential for
 ubiquitin ligase activity. It coordinates an additional third zinc
 atom.
 CC -!- SIMILARITY: Belongs to the RBX1 family.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AL138639; CAB87200.1; --
 DR F1R; T47341; T47341.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 KW Hypothetical protein; Metal-binding; Nuclear protein;
 KW Ub1 conjugation pathway; Zinc; Zinc-finger.
 FT ZING 60 107 RING-type.
 FT METAL 49 49 Zinc 1 (By similarity).
 FT METAL 52 52 Zinc 1 (By similarity).
 FT METAL 60 60 Zinc 3 (By similarity).
 FT METAL 63 63 Zinc 3 (By similarity).
 FT METAL 75 75 Zinc 3 (By similarity).
 FT METAL 82 82 Zinc 2 (By similarity).
 FT METAL 84 84 Zinc 2 (By similarity).
 FT METAL 87 87 Zinc 1 (By similarity).
 FT METAL 89 89 Zinc 3 (By similarity).
 FT METAL 90 90 Zinc 1 (By similarity).
 FT METAL 101 101 Zinc 2 (By similarity).
 FT METAL 104 104 Zinc 2 (By similarity).
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 Matches 88; Conservative 5; Mismatches 13; Indels 2; Gaps 1;
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 DB 10 MGESSSISVPS--SSSKNSKRFELKKWSAVALWWDIVVDNCAICRNHMDLCIECLANQ 67
 QY 61 ASATSECTVAMGVCMHAFHFCISRWLKTQVCPDLNREWEFKYGH 108
 DB 68 ASATSECTVAMGVCMHAFHFCISRWLKTQVCPDLNREWEFKYGH 115

RESULT 14
 RBX1 CAEBL STANDARD; PRT; 110 AA.
 AC Q23457; Q8WSQ1;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE RING-box protein 1 (Rbx1) (Ce-rbx-1).
 GN Name=rbx-1; ORFNames=ZK287.5;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG "The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE OF 2-110 FROM N.A.
 RS Sasagawa Y., Urano T., Kohara Y., Takahashi H., Higashitanai A.;
 RA "Characterization of rbx1 gene from Caenorhabditis elegans.";
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Component of the SCF (SKP1-CUL1-F-box protein) E3
 CC ubiquitin ligase complex, which mediates the ubiquitination and
 CC subsequent proteasomal degradation of target proteins. Through the
 CC RING-type zinc finger, seems to recruit the E2 ubiquitination
 CC enzyme to the complex and brings it into close proximity to the
 CC substrate (By similarity).
 CC -!- PATHWAY: Ubiquitin conjugation; third step.
 CC -!- SUBUNIT: Part of SCF complexes, which consist of a SKP1 or a SKP1-
 CC related protein, a cullin protein, and a F-box protein (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC -!- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity. It coordinates an additional third zinc
 CC atom.
 CC -!- SIMILARITY: Belongs to the RING-box family.
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.
 CC -!- CAUTION: It is uncertain whether Met-1 or Met-10 is the initiator.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z70757; CA94801.1; -;
 DR EMBL; AB077287; BAB83695.1; ALT INIT.
 DR PIR; T27823; T27823.
 DR WormBase; WBGene0004320; rbx-1.
 DR WormPep; ZK287.5; CE06614.
 DR InterPro; IPR001841; Znf_ring.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 DR PROSITE; PS50089; ZF_RING_2; 1.
 DR Metal-binding; Nuclear protein; Ubl conjugation pathway; Zinc;
 KW Zinc-finger.
 FT ZN_FING 44 100 RING-type.
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 FT METAL 47 47 Zinc 1 (By similarity).
 FT METAL 55 55 Zinc 3 (By similarity).
 FT METAL 58 58 Zinc 3 (By similarity).
 FT METAL 70 70 Zinc 3 (By similarity).
 FT METAL 77 77 Zinc 2 (By similarity).
 FT METAL 79 79 Zinc 2 (By similarity).
 FT METAL 82 82 Zinc 3 (By similarity).
 FT METAL 84 84 Zinc 3 (By similarity).
 FT METAL 85 85 Zinc 1 (By similarity).
 FT METAL 96 96 Zinc 2 (By similarity).
 FT METAL 99 99 Zinc 2 (By similarity).
 FT CONFLICT 2 3 AQ -> GP (in Ref. 2).
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 Best Local Similarity 79.3%; Pred. No. 3.6e-47;
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 1 MAQASDSTAMEVEATNTQTV-KRFEVKKNSAVALWWDVVDNCAICRNHIMDLICBQ 59
 58 ANQASATSEECTVAVGNCNHAFFHCISRWLKTQVCPDNRNWEFQYKGH 108

DB 60 ANQAGLKDCECTVAVGNCNHAFFHCISRWLKTQVCPDNRNWEFQYKGH 110
 RESULT 15
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 ID REX1 SCHPO STANDARD; PRT; 107 AA.
 AC O13959;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE RING-box protein p1p1 (Pop-interacting protein 1) (RING-box protein
 DE 1).
 GN Name=p1p1; ORFNames=SPAC23H4.18c;
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND INTERACTIONS
 RP WITH POP1, POP2 AND PCUL1.
 RX MEDLINE=22325332; PubMed=12167173; DOI=10.1186/1472-2091-3-22;
 RA Seibert V., Prohl C., Schoultz I., Rhee E., Lopez R., Abderazzaq K.,
 RA Zhou C., Wolf D.A.;
 RA "Combinatorial diversity of fission yeast SCF ubiquitin ligases by
 RT homo- and heterooligomeric assemblies of the F-box proteins Pop1 and
 RT Pop2p.";
 RL BMC Biochem. 3:22-22(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Spours J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Girdles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -!- FUNCTION: Component of E3 ubiquitin ligase SCF complexes, which
 CC mediate the ubiquitination and subsequent proteasomal degradation
 CC of target proteins. Seems to recruit the E2 ubiquitination enzyme,
 CC like UBC3/CDC34, to the complex and brings it into close proximity
 CC to the substrate.
 CC -!- PATHWAY: Ubiquitin conjugation; third step.
 CC -!- SUBUNIT: Part of a SCF E3 ubiquitin ligase complex containing
 CC psh1, p1p1, pcul1 and the F-box proteins pop1 and pop2. Instead of
 CC the pop1/pop2 heterodimer also homooligomers of pop1 or pop2 may
 CC be present in the complex.
 CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.
 CC -!- DOMAIN: The RING-type zinc finger domain is essential for
 CC ubiquitin ligase activity. It coordinates an additional third zinc
 CC atom.

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OM nucleic - nucleic search, using sw model

Run on: June 24, 2005, 00:17:37 ; Search time 2063 Seconds
(without alignments)
7680.492 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: gb_om.*
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8: gb_pi.*
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11: gb_ats.*
12: gb_av.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	327	100.0	433	6 CQ698451	CQ698451 Sequence
3	327	100.0	453	6 CQ690099	CQ690099 Sequence
4	327	100.0	467	6 CQ695007	CQ695007 Sequence
5	327	100.0	471	6 CQ712328	CQ712328 Sequence
6	327	100.0	472	6 CQ711142	CQ711142 Sequence
7	327	100.0	482	6 AX888031	AX888031 Sequence
8	327	100.0	482	6 BD027641	BD027641 Sequence
9	327	100.0	507	6 CQ729899	CQ729899 Sequence
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15	327	100.0	554	9 BC017370	BC017370 Homo sapi
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17	316	96.6	430	6 CQ709825	CQ709825 Sequence
18	308.8	94.4	4476	6 CQ493737	CQ493737 Sequence
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	36	253.6	77.6	3208	6	AR542209	AR542209 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS AF142059 327 bp mRNA linear PRI 14-JUL-1999
DEFINITION Homo sapiens RING finger protein (ROC1) mRNA, complete cds.
ACCESSION AF142059
VERSION AF142059.1 GI:4809215
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 327)
Ohta, T., Michel, J.J., Schottelius, A.J. and Xiong, Y.
AUTHORS ROC1, a homolog of APC11, represents a family of cullin partners
TITLE with an associated ubiquitin ligase activity
JOURNAL Mol. Cell 3 (4), 535-541 (1999)
MEDLINE 99247022
PUBMED 10230407
REFERENCE 2 (bases 1 to 327)
Ohta, T., Michel, J.J. and Xiong, Y.
AUTHORS Direct Submission
TITLE Submitted (10-APR-1999) Lineberger Comprehensive Cancer Center,
JOURNAL University of North Carolina at Chapel Hill, Mason Farm Rd. and
Manning Dr., Chapel Hill, NC 27599-7295, USA

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FQKYGH"


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REFERENCE
AUTHORS      Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE        Compositions and methods relating to osteoarthritis
JOURNAL      Patent: WO 02070737-A 39933 12-SEP-2002;
              Chondrogene Inc. (CA)
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Best Local Similarity 100.0%; Pred. No. 1.4e-90;
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QY 1 ATGGCGGCGAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
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DB 140 AACTGTGCATCTCGCTGGTCTCAAAACACAGCAGGTGTGTCCATTGGACAAACAGAG 199
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DEFINITION     Sequence 57254 from Patent WO02070737.
ACCESSION      CQ712328
VERSION        CQ712328.1 GI:42273185
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS        Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE          Compositions and methods relating to osteoarthritis
JOURNAL        Patent: WO 02070737-A 57254 12-SEP-2002;
               Chondrogene Inc. (CA)
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QY 61 CGCTTTGAAGTGAAAAAGTGGATGAGTCCCTCTGGGCTGGGATATTGTGTTGAT 120
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Db 77 CGCTTTGAAGTGAAAAAGTGGATGAGTCCCTCTGGGCTGGGATATTGTGTTGAT 136
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DB 257 TTCACACTGCATCTCGCTGGTCTCAAAACACAGCAGGTGTGTCCATTGGACAAACAGAG 316
QY 301 TGGGAATTCAAAAAGTATGGGCACCTAG 327
DB 317 TGGGAATTCAAAAAGTATGGGCACCTAG 343
RESULT 6
LOCUS          CQ711142          472 bp      DNA      linear      PAT 03-FEB-2004
DEFINITION     Sequence 56068 from Patent WO02070737.
ACCESSION      CQ711142
VERSION        CQ711142.1 GI:42271999
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS        Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE          Compositions and methods relating to osteoarthritis
JOURNAL        Patent: WO 02070737-A 56068 12-SEP-2002;
               Chondrogene Inc. (CA)
FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.4e-90;
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DB 80 CGCTTTGAAGTGAAAAAGTGGATGAGTCCCTCTGGGCTGGGATATTGTGTTGAT 139
QY 121 AACTGTGCATCTCGAGGAACCAATTATGGATCTTTGATAGAAATGTCAAGCTAACCAAG 180
DB 140 AACTGTGCATCTCGAGGAACCAATTATGGATCTTTGATAGAAATGTCAAGCTAACCAAG 199
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AX888031
LOCUS AX888031 482 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 3894 from Patent EPI033401.
ACCESSION AX888031
VERSION AX888031.1 GI:40046785
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 3894 06-SEP-2000;
Genset (FR)
FEATURES
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CDS
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Best Local Similarity 100.0%; Pred. No. 1.4e-90;
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DB 29 ATGGCGCAGCATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 88
QY 61 CGCTTTGAAGTGAAGTGGATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT 120
DB 89 CGCTTTGAAGTGAAGTGGATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT 148
QY 121 AACTGTGCCATCTGCAGAACCACTATTATGGATCTTTTGCATAGAAATGTCAGCTAACCCAG 180
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DB 209 GCGTCCGCTACTTCAGAAAGTGGATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT 268
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DB 269 TTCACATGCATCTCGCTGGCTCAAAACACGACAGGTGTCCATTGGACACACAGAG 328
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DB 329 TGGGAATTCCTCAAAAGTATGGCACTAG 355
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LOCUS BD027641 482 bp DNA linear PAT 27-AUG-2002
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD027641
VERSION BD027641.1 GI:22569383
KEYWORDS JP 2001269182-A/3887.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
TITLE Sequence tag and encoded human protein

JOURNAL Patent: JP 2001269182-A 3887 02-OCT-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/3887
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
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FT CDS Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 CGCTTTGAAGTGAAGTGGATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT 120
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QY 181 GCGTCCGCTACTTCAGAAAGTGGATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT 240
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DB 269 TTCACATGCATCTCGCTGGCTCAAAACACGACAGGTGTCCATTGGACACACAGAG 328
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DB 329 TGGGAATTCCTCAAAAGTATGGCACTAG 355
RESULT 9
CQ729899
LOCUS CQ729899 507 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 15833 from Patent WO02068579.
ACCESSION CQ729899
VERSION CQ729899.1 GI:42302243
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
human exons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 15833 06-SEP-2002;
PB Corporation (NY) (US)
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source Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 1.4e-90;
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QY 121 AACTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGATGTCAAGCTAACCCAG 180
DB 127 AACTGTGCCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGATGTCAAGCTAACCCAG 186
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DB 187 GGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACATGCTTTTCAC 246
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QY 301 TGGGAATTCCTCAAAAGTATGGGCACCTAG 327
DB 307 TGGGAATTCCTCAAAAGTATGGGCACCTAG 333

RESULT 10
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LOCUS      VonHippel-Lindau tumor suppressor complex and novel component of
DEFINITION      SCF ubiquitin ligase.
ACCESSION      BD271520.1 GI:33081288
VERSION      BD271520.1
KEYWORDS      JP 2002541775-A/1.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheraia; Primates; Catarrhini; Hominiidae; Homo.
TITLE      Conaway, J.W., Conaway, R.C. and Kamura, T.
      VonHippel-Lindau tumor suppressor complex and novel component of
      SCF ubiquitin ligase
JOURNAL      Patent: JP 2002541775-A 1 10-DEC-2002;
COMMENT      OKLAHOMA MEDICAL RESEARCH FOUNDATION
      OS      Homo sapiens (human)
      PN      JP 2002541775-A/1
      PD      10-DEC-2002
      PF      25-FEB-2000 JP 2000601023
      PR      28-FEB-1999 US 60/121787
      PI      JOAN W CONAWAY, RONALD C CONAWAY, TAKUMI KAMURA PC
      C12N15/09, A61K38/00, A61K38/53, A61K45/00, A61P35/00, C07K14/47, PC
      C12N1/15,
      PC
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Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGAGCGATGGATGGATATACCCCGAGCGGACCAACAGCGGCGCGGCAAGAG 60
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DB 67 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 126
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DB 247 TTCCACTGCATCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGAG 306
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DB 307 TGGGAATTCCTCAAAAGTATGGGCACCTAG 333

RESULT 11
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LOCUS      Homo sapiens ring-box protein 1 (RBX1) mRNA, complete cds.
DEFINITION      AF140598
ACCESSION      AF140598
VERSION      AF140598.1 GI:4769003
KEYWORDS      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheraia; Primates; Catarrhini; Hominiidae; Homo.
TITLE      Kamura, T., Koepf, D.M., Conrad, M.N., Skowrya, D., Moreland, R.J.,
      Iliopoulos, O., Lane, W.S., Kaelin, W.G. Jr., Ellledge, S.J.,
      Conaway, R.C., Harper, J.W. and Conaway, J.W.
      Rbx1, a component of the VHL tumor suppressor complex and SCF
      ubiquitin ligase
JOURNAL      Science 284 (5414), 657-661 (1999)
COMMENT      99234320
      PUBMED      10213691
      REFERENCE      2 (bases 1 to 508)
      AUTHORS      Kamura, T., Lane, W.S., Conaway, R.C. and Conaway, J.W.
      TITLE      Direct Submission
      JOURNAL      Submitted (05-APR-1999) Prog. Molec. Cell Biol., HHMI, Oklahoma
      Med. Res. Fdn., 825 NE 13th St, Oklahoma City, OK 73104, USA
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Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E.B. Consortium/LLNL at: <http://image.llnl.gov>
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QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 120
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QY 121 AACTGTGCCATCTGCAGGAACCACTATTATGATCTTTGCATAGATGTCAGCTAACCCAG 180
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DB 306 TGGGAATTCCTCAAAAGTATGGGCACCTAG 332

RESULT 14

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LOCUS
DEFINITION
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(cDNA clone C22ORF:pGEM.RBX1).
ACCESSION
CR456560
VERSION
CR456560.1 GI:47678650
KEYWORDS
CDNA; chromosome 22; ORF.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

The Wellcome Trust Sanger Institute program to isolate cDNA clones representing the full length open reading frame of well annotated protein coding genes on human chromosome 22. For more information see <http://www.sanger.ac.uk/HGP/Chr22/>.

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Best Local Similarity 100.0%; Pred. No. 1.4e-90; Mismatches 0; Indels 0; Gaps 0;
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RESULT 15

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LOCUS
DEFINITION
Homo sapiens ring-box 1, mRNA (cDNA clone IMAGE:4065797), partial cds.
ACCESSION
BC017370
VERSION
BC017370.1 GI:16924201
KEYWORDS
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 535)
Collins, J.E., Wright, C.L., Edwards, C.A., Davis, M.P., Grinham, J.A., Cole, C.G., Goward, M.E., Aguado, B., Mallia, M., Mokrab, Y., Huckle, E.J., Beare, D.M. and Dunham, I.

Submitted (24-MAY-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: c22g@sanger.ac.uk Manuscript Sanger Institute name: pGEM.RBX1

Homo sapiens cDNA sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to isolate cDNA clones representing the full length open reading frame of well annotated protein coding genes on human chromosome 22. For more information see <http://www.sanger.ac.uk/HGP/Chr22/>.

Location/Qualifiers

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 18:42:59 ; Search time 359 Seconds
(without alignments)
5392.076 Million cell updates/sec

Title: US-09-541-462B-1

Perfect score: 327

Sequence: 1 atggcgagcgatgatgt.....tccaaaagatgggcactag 327

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

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5: Geneseqn2001bs.*

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9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	327	100.0	508	13	ACN40951 Tumour-as
8	325	99.4	476	9	ACH29979 Human tes
9	321.8	98.4	3726	13	ADSO9913 Human the
10	321.8	98.4	4543	11	ACN90161 Breast ca
11	320	97.9	503	12	ADQ92179 Human aut
12	308.8	94.4	4476	5	ABV25615 Human pro
13	302.4	92.5	380	8	ABX39512 Bovine ES
14	301.2	92.1	5347	6	AAS94844 Human DNA
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17	296.8	90.8	3484	13	ADQ80865 Human SPA
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36	184.6	56.5	731	10	ADK56881	ADK56881 Plant DNA
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40	182.8	55.9	527	10	ADK56883	ADK56883 Plant DNA
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44	175.6	53.7	691	10	ADK56880	ADK56880 Plant DNA
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ALIGNMENTS

RESULT 1

AAA96882

ID AAA96882 standard; DNA; 327 BP.

XX

AC AAA96882;

DT 19-FEB-2001 (first entry)

DE Nucleotide sequence of human ring finger protein ROC1.

XX

KW ROC1; ROC2; cullin; ring finger protein; APC11; APC complex; SCF pathway;

KW cullin dependent ubiquitin ligase; CDK inhibitor Sic1 degradation;

KW tumour; ss.

XX

OS Homo sapiens.

XX

FH Key

FT CDS

FT

FT

FT

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

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XX

XX

XX

XX

XX

CC The present sequence encodes a human ROC1 ring finger protein. The
CC specification also describes human ROC2. ROC1 and ROC2 are similar to
CC APC11, a subunit of the APC complex. The proteins stimulate cullin
CC dependent ubiquitin ligase activity. ROC1 functions in vivo as an
CC essential regulator of CDK inhibitor Sic1 degradation by the SCF
CC (undefined) pathway. ROC proteins are useful for screening bioactive
CC agents that interfere with the binding of ROC proteins with cullin
CC proteins. Pharmaceutical formulations comprising ROC proteins are useful
CC for diagnostic and therapeutic purposes, preferably for diagnosing and
CC treating tumours
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Best Local Similarity 100.0%; Pred. No. 3.5e-101;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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ID AAC03896 standard; cDNA; 482 BP.
XX AAC03896;
XX 06-OCT-2000 (first entry)
XX Human secreted protein 5' EST, SEQ ID NO: 3894.
DE
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX Homo sapiens.
XX EP1033401-A2.
XX 06-SEP-2000.
XX 21-FEB-2000; 2000EP-00200610.
XX 26-FEB-1999; 99US-0122487P.
XX (GEST) GENSET.
XX Dumas Milne Edwards J, Duclert A, Giordano J;
PI
XX
XX WPI; 2000-500381/45.
DR P-PSDB; AAG03890.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for

PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX Claim 1; SEQ ID NO 3894; 71pp + Sequence Listing; English.
PS
XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. An ORF has been identified within the
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC derived from 30 different tissues. EST sequences usually correspond
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC well suited for isolating cDNA sequences derived from the 5' ends of
CC mRNAs and even in those cases where longer cDNA sequences have been
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC mRNAs with intact 5' ends and can therefore be used to obtain full length
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC gene therapy and chromosome mapping procedures. They are used to obtain
CC upstream regulatory sequences and to design expression and secretion
CC vectors
XX
SQ Sequence 482 BP; 116 A; 103 C; 121 G; 140 T; 0 U; 2 Other;
Query Match 100.0%; Score 327; DB 3; Length 482;
Best Local Similarity 100.0%; Pred. No. 4.3e-101;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGCAAGAAG 60
DB 29 ATGCGCGCAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGCAAGAAG 88
QY 61 CGCTTTGAAGTGAAGTGAATGCAGTACGATGATGATCTTGGCATAGATTTGGTGTGAT 120
DB 89 CGCTTTGAAGTGAAGTGAATGCAGTACGATGATGATCTTGGCATAGATTTGGTGTGAT 148
QY 121 AACTGTGCCATCTGCAGGAACCAACATATGATGATCTTGCATAGATGTCAAGCTAACCCAG 180
DB 149 AACTGTGCCATCTGCAGGAACCAACATATGATGATCTTGCATAGATGTCAAGCTAACCCAG 208
QY 181 GCCTCCGCTACTTCAAGAAGTGTACTGTCCGATGGGGAGTCTGTAAACCATGCTTTTCAC 240
DB 209 GCCTCCGCTACTTCAAGAAGTGTACTGTCCGATGGGGAGTCTGTAAACCATGCTTTTCAC 268
QY 241 TTCCACTGCATCTCGCTGGCTCAAAACACGACAGGTGTCCATTGGACACAGAGAG 300
DB 269 TTCCACTGCATCTCGCTGGCTCAAAACACGACAGGTGTCCATTGGACACAGAGAG 328
QY 301 TGGGAATTCAAAAGTATGGCACTAG 327
DB 329 TGGGAATTCAAAAGTATGGCACTAG 355
RESULT 3
ADQ87496
ID ADQ87496 standard; cDNA; 506 BP.
XX ADQ87496;
XX 07-OCT-2004 (first entry)
XX Human tumour-associated antigenic target (TAT) cDNA sequence #4374.
DE
XX
XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX Homo sapiens.
XX WO2004060270-A2.
XX 22-JUL-2004.
XX 15-OCT-2003; 2003WO-US029126.
XX 18-OCT-2002; 2002US-0418988P.
XX

XX (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
XX
PI Wu TD, Zhou Y;
XX WPI; 2004-534300/51.
DR
XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX
PS Claim 1; SEQ ID NO 4374; 5504pp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the
CC presence of a protein in a sample suspected of containing the protein
CC described above; (15) methods of diagnosing the presence of a tumour in a
CC mammal; (16) a method for treating or preventing a cell proliferative
CC disorder associated with increased expression or activity of the above
CC protein; and (17) a method of binding an antibody, oligopeptide or
CC organic molecule to a cell that expresses the protein described above.
CC The TAT sequences have cytostatic activities, and can be used in gene
CC therapy. The composition and methods are useful for diagnosing,
CC preventing or treating cancer. The composition is also used for preparing
CC a medicament for the therapeutic treatment or diagnostic detection of a
CC cell proliferative disorder or cancer. The present sequence represents a
CC human TAT cDNA sequence from the present invention.
XX
SQ Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;

Query Match
Best Local Similarity 100.0%; Score 327; DB 12; Length 506;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGAGCGATGGATGTGATACCCGAGCGGACCAACAGCGCGCGGCAAGAAG 60
DB 6 ATGGCGGAGCGATGGATGTGATACCCGAGCGGACCAACAGCGCGCGGCAAGAAG 65
QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
DB 66 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 125
QY 121 AACTGTGCCATCTGAGGAGCAACACATATGATCTTTGCATAGATGTCAACCTAACACAG 180
DB 126 AACTGTGCCATCTGAGGAGCAACACATATGATCTTTGCATAGATGTCAACCTAACACAG 185
QY 181 GCGTCGCGTACTTCAGAGAGGTGTACTGTCGATCGGAGGTCTGTAAACATGCTTTTAC 240

Db 186 GCGTCGCGTACTTCAGAGAGGTGTACTGTCGATCGGAGGTCTGTAAACATGCTTTTAC 245
QY 241 TTCCACTGCGATCTCTCGCTGGCTCAAAACAGCAGGAGTGTCTCCATTGGACAAACAGAGAG 300
Db 246 TTCCACTGCGATCTCTCGCTGGCTCAAAACAGCAGGAGTGTCTCCATTGGACAAACAGAGAG 305
QY 301 TGGGAATTCCTCAAAAGATATGGGCACTAG 327
Db 306 TGGGAATTCCTCAAAAGATATGGGCACTAG 332

RESULT 4
ADQ87156
ID ADQ87156 standard; cDNA; 506 BP.
XX
AC ADQ87156;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4032.
XX
KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW cancer; cell proliferative disorder; gene; ss.
XX
OS Homo sapiens.
XX
FN WO2004060270-A2.
XX
PD 22-JUL-2004.
XX
PF 15-OCT-2003; 2003WO-US029126.
XX
PR 18-OCT-2002; 2002US-0418988P.
XX
PA (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
XX
XX Wu TD, Zhou Y;
XX WPI; 2004-534300/51.
XX
XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
XX preventing or treating cell proliferative disorders such as cancer.
XX
XX Claim 1; SEQ ID NO 4032; 5504pp; English.
XX
CC The present invention describes an isolated tumour-associated antigenic
CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
CC (c). Also described: (1) an expression vector comprising the above
CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC a process for producing a polypeptide; (4) an isolated polypeptide
CC comprising: (a) an amino acid sequence encoded by any of the above
CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC length coding region of the above nucleotide sequences; or (c) a sequence
CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC an isolated antibody that binds to the above polypeptide; (7) a process
CC for producing the antibody; (8) an isolated oligopeptide that binds to
CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC binding organic molecule that binds to the above polypeptide; (10) a
CC composition of matter comprising the above (chimeric) polypeptide,
CC antibody, oligopeptide or TAT binding organic molecule, in combination
CC with a carrier; (11) an article of manufacture comprising a container and
CC the composition of matter contained within the container; (12) methods of
CC inhibiting the growth of a cell that expresses the above protein, where
CC the growth of the cell is at least in part dependent upon a growth
CC potentiating effect of the above protein; (13) a method of
CC therapeutically treating a mammal having a cancerous tumour comprising
CC cells that express the above protein; (14) a method of determining the

CC presence of a protein in a sample suspected of containing the protein
 CC described above; (15) methods of diagnosing the presence of a tumour in a
 CC mammal; (16) a method for treating or preventing a cell proliferative
 CC disorder associated with increased expression or activity of the above
 CC protein; and (17) a method of binding an antibody, oligopeptide or
 CC organic molecule to a cell that expresses the protein described above.
 CC The TAT sequences have cytostatic activities, and can be used in gene
 CC therapy. The composition and methods are useful for diagnosing,
 CC preventing or treating cancer. The composition is also used for preparing
 CC a medicament for the therapeutic treatment or diagnostic detection of a
 CC cell proliferative disorder or cancer. The present sequence represents a
 CC human TAT cDNA sequence from the present invention.

XX Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 327; DB 12; Length 506;
 Best Local Similarity 100.0%; Pred. No. 4.4e-101;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGCGGCGAGCGATGGATGGATACCCCGAGCGGACCAACAGCGCGCGGCGCAAGAAG 60
 DB |||||||
 QY 6 ATGGCGGCGAGCGATGGATGGATACCCCGAGCGGACCAACAGCGCGCGGCGCAAGAAG 65
 DB |||||||
 QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
 DB |||||||
 QY 66 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 125
 DB |||||||
 QY 121 AACTGTGCCATCTGCAGAACCAACATATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 DB |||||||
 QY 126 AACTGTGCCATCTGCAGAACCAACATATGATGATGATGATGATGATGATGATGATGATGATGAT 185
 DB |||||||
 QY 181 GCGTCGCGTACTTTCAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 240
 DB |||||||
 QY 186 GCGTCGCGTACTTTCAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 245
 DB |||||||
 QY 241 TTCCACTGTCATCTCTCGCTGGCTTCAAAACACAGCAGGTGTGTCCATTGGACCAACAGAGAG 300
 DB |||||||
 QY 246 TTCCACTGTCATCTCTCGCTGGCTTCAAAACACAGCAGGTGTGTCCATTGGACCAACAGAGAG 305
 DB |||||||
 QY 301 TGGGAATTCAAAAGTATGGCACTAG 327
 DB |||||||
 QY 306 TGGGAATTCAAAAGTATGGCACTAG 332
 DB |||||||

RESULT 5
 ADQ84881
 ID ADQ84881 standard; cDNA; 506 BP.
 AC ADQ84881;
 DT 07-OCT-2004 (first entry)
 XX Human tumour-associated antigenic target (TAT) cDNA sequence #1695.
 DE human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
 XX cancer; cell proliferative disorder; gene; ss.
 KW Homo sapiens.
 XX OS
 XX WO2004060270-A2.
 PN 22-JUL-2004.
 PD 15-OCT-2003; 2003WO-US029126.
 XX 18-OCT-2002; 2002US-0418988P.
 XX (GETH) GENENTECH INC.
 PA (WUTD/) WU T D.
 PA (ZHOU/) ZHOU Y.
 XX WU TD, Zhou Y;
 PI WU TD, Zhou Y;
 XX

DR WPI; 2004-534300/51.
 XX New nucleic acid molecule and encoded polypeptide, for diagnosing,
 PT preventing or treating cell proliferative disorders such as cancer.
 XX Claim 1; SEQ ID NO 1695; 5504pp; English.
 PS The present invention describes an isolated tumour-associated antigenic
 CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
 CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
 CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
 CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-
 CC (c). Also described: (1) an expression vector comprising the above
 CC nucleic acid; (2) a host cell comprising the above expression vector; (3)
 CC a process for producing a polypeptide; (4) an isolated polypeptide
 CC comprising: (a) an amino acid sequence encoded by any of the above
 CC nucleotide sequences; (b) an amino acid sequence encoded by the full-
 CC length coding region of the above nucleotide sequences; or (c) a sequence
 CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
 CC comprising the above polypeptide fused to a heterologous polypeptide; (6)
 CC an isolated antibody that binds to the above polypeptide; (7) a process
 CC for producing the antibody; (8) an isolated oligopeptide that binds to
 CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)
 CC binding organic molecule that binds to the above polypeptide; (10) a
 CC composition of matter comprising the above (chimeric) polypeptide,
 CC antibody, oligopeptide or TAT binding organic molecule, in combination
 CC with a carrier; (11) an article of manufacture comprising a container and
 CC the composition of matter contained within the container; (12) methods of
 CC inhibiting the growth of a cell that expresses the above protein, where
 CC the growth of the cell is at least in part dependent upon a growth
 CC potentiating effect of the above protein; (13) a method of
 CC therapeutically treating a mammal having a cancerous tumour comprising
 CC cells that express the above protein; (14) a method of determining the
 CC presence of a protein in a sample suspected of containing the protein in a
 CC mammal; (15) methods of diagnosing the presence of a tumour in a
 CC disorder associated with increased expression or activity of the above
 CC protein; and (17) a method of binding an antibody, oligopeptide or
 CC organic molecule to a cell that expresses the protein described above.
 CC The TAT sequences have cytostatic activities, and can be used in gene
 CC therapy. The composition and methods are useful for diagnosing,
 CC preventing or treating cancer. The composition is also used for preparing
 CC a medicament for the therapeutic treatment or diagnostic detection of a
 CC cell proliferative disorder or cancer. The present sequence represents a
 CC human TAT cDNA sequence from the present invention.

XX Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 327; DB 13; Length 506;
 Best Local Similarity 100.0%; Pred. No. 4.4e-101;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGCGGCGAGCGATGGATGGATACCCCGAGCGGACCAACAGCGCGCGGCGCAAGAAG 60
 DB |||||||
 QY 6 ATGGCGGCGAGCGATGGATGGATACCCCGAGCGGACCAACAGCGCGCGGCGCAAGAAG 65
 DB |||||||
 QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
 DB |||||||
 QY 66 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 125
 DB |||||||
 QY 121 AACTGTGCCATCTGCAGAACCAACATATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 DB |||||||
 QY 126 AACTGTGCCATCTGCAGAACCAACATATGATGATGATGATGATGATGATGATGATGATGATGAT 185
 DB |||||||
 QY 181 GCGTCGCGTACTTTCAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 240
 DB |||||||
 QY 186 GCGTCGCGTACTTTCAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 245
 DB |||||||
 QY 241 TTCCACTGTCATCTCTCGCTGGCTTCAAAACACAGCAGGTGTGTCCATTGGACCAACAGAGAG 300
 DB |||||||
 QY 246 TTCCACTGTCATCTCTCGCTGGCTTCAAAACACAGCAGGTGTGTCCATTGGACCAACAGAGAG 305
 DB |||||||
 QY 301 TGGGAATTCAAAAGTATGGCACTAG 327

Db		306	TGGGAATTC	AAAGATG	TGGGCACTAG	332
RESULT 6						
AAA74978						
ID	AAA74978	standard; DNA; 508 BP.				
XX	AC	AAA74978;				
XX	AC					
DT	DT	02-JAN-2001 (first entry)				
XX						
DE		DNA encoding a human cullin-interacting RING-H2 finger protein (Rbx1).				
XX						
KW		Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;				
KW		tumour suppressor; carcinoma; Ring box associated carcinoma;				
KW		von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;				
KW		cerebellar hemangioblastoma; hemangioma; retinal angiomas;				
KW		pheochromocytomas; ss.				
XX						
OS		Homo sapiens.				
XX						
PH	Key	Location/Qualifiers				
FT	CDS	7..333				
FT		/*tag= a				
FT		/product= "cullin-interacting RING-H2 finger protein				
FT		(Rbx1)"				
XX						
PN	W0200050445-Al.					
XX						
PD	31-AUG-2000.					
XX						
PP	25-FEB-2000; 2000WO-US004838.					
XX						
PR	26-FEB-1999; 99US-0121787P.					
XX						
XX	(OKLA-) OKLAHOMA MEDICAL RES FOUND.					
PA						
XX						
PI	Conaway JA, Conaway RC, Kamura T;					
XX						
DR	WPI; 2000-572067/53.					
DR	P-PSDB; AAB08813.					
XX						
PT	Cullin interacting RING-H2 finger protein, a component of von Hippel-					
PT	Lindau tumor suppressor complex and Skp1-Cdc5p-P-box protein (SCF)					
PT	ubiquitin ligase, useful for diagnosing and treating Ring box protein					
PT	associated carcinomas.					
XX						
PS	Claim 3; Page 35; 37pp; English.					
XX						
CC	The present sequence encodes a human cullin-interacting RING-H2 finger					
CC	protein (Ring box protein), designated Rbx1. The polypeptide is a tumour					
CC	suppressor. Rbx1 is useful for diagnosing a predisposition of a patient					
CC	to certain carcinomas. It is also useful for treating Ring box protein					
CC	associated carcinomas or augmenting metabolically deficient system in					
CC	animals. Rbx1 is also useful for evaluating the effectiveness of a					
CC	therapeutic treatment for Ring box associated carcinomas. Rbx1 can be					
CC	used to screen for agents which augment or inhibit the activity of other					
CC	cullin-containing ubiquitin ligase and of the VHL (von Hippel-Lindau)					
CC	complex controlling the conjugation of ubiquitin or ubiquitin-like					
CC	proteins to various sets of target proteins. Carcinomas which may be					
CC	treated include renal carcinomas, cerebellar hemangioblastomas and					
CC	hemangiomas, retinal angiomas and pheochromocytomas					
XX						
SQ	Sequence 508 BP; 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other;					
	Query Match	100.0%;	Score 327;	DB 3;	Length 508;	
	Best Local Similarity	100.0%;	Pred. No. 4.4e-101;			
	Matches 327;	Conservative	0;	Mismatches	0;	Gaps 0;
Qy	1	ATGCGGAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAG	60			
Db	7	ATGCGGAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAG	66			

CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT nucleic acid of the invention
 XX
 XX Sequence 508 BP; 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other;

Query Match 100.0%; Score 327; DB 13; Length 508;
 Best Local Similarity 100.0%; Pred. No. 4.4e-101;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGAGCGATGGATGGATACCCGAGCGGCCACCAACAGCGCGCGGCAAGAG 60
 Db ATGGCGGCGAGCGATGGATGGATACCCGAGCGGCCACCAACAGCGCGCGGCAAGAG 66
 QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
 Db CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 126
 QY 121 AACTGTGCGATCTGCAGGACCAACATATGGATCTTTGCATAGAAATGTCAGTACAC 180
 Db AACTGTGCGATCTGCAGGACCAACATATGGATCTTTGCATAGAAATGTCAGTACAC 186
 QY 181 GCGTCGCGTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACATGCTTTTCAC 240
 Db GCGTCGCGTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACATGCTTTTCAC 246
 QY 241 TTCCACTGCACTCTCGCTGGCTCAAAACACAGAGTGTGTCATTTGACCAACAGAGAG 300
 Db TTCCACTGCACTCTCGCTGGCTCAAAACACAGAGTGTGTCATTTGACCAACAGAGAG 306
 QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
 Db TGGGAATTCAAAAGTATGGGCACTAG 333

RESULT 8
 ACH29979
 ID ACH29979 standard; cDNA; 476 BP.
 XX
 AC ACH29979;
 AC
 DT 13-OCT-2003 (first entry)
 XX
 DE Human testis cDNA #365.
 XX
 KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
 KW genome mapping; biodiversity; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 XX US2003073623-A1.
 PN 17-APR-2003.
 XX
 PD 30-JUL-2001; 2001US-00918995.
 XX
 PF 30-JUL-2001; 2001US-00918995.
 XX
 PR (DRMA/) DRMANAC R T.
 XX (LABA/) LABAT I.
 XX (STAC/) STACHE-CRAIN B.
 XX (DICK/) DICKSON M C.
 XX (JONE/) JONES L W.
 XX Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;

XX WPI; 2003-615964/58.
 XX New polynucleotide sequences obtained from various cDNA libraries, useful
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.
 XX
 PS Claim 1; SEQ ID NO 17191; 44pp; English.
 XX
 CC The invention relates to an isolated polynucleotide comprising any one of
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antisense DNA or RNA. The purified polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030073623
 XX
 XX Sequence 476 BP; 119 A; 111 C; 124 G; 118 T; 0 U; 4 Other;

Query Match 99.4%; Score 325; DB 9; Length 476;
 Best Local Similarity 100.0%; Pred. No. 2.1e-100;
 Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGCGCAGCGATGGATGGATACCCGAGCGGCCACCAACAGCGCGCGGCAAGAGCG 62
 Db GCGCGCAGCGATGGATGGATACCCGAGCGGCCACCAACAGCGCGCGGCAAGAGCG 133
 QY 63 CTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 122
 Db CTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 193
 QY 123 CTGTGCGATCTGCAGAACCAACATATGGATCTTTGCATAGAAATGTCAGTACACGCG 182
 Db CTGTGCGATCTGCAGAACCAACATATGGATCTTTGCATAGAAATGTCAGTACACGCG 253
 QY 183 GTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACATGCTTTTCAC 242
 Db GTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACATGCTTTTCAC 313
 QY 243 CCACTGCACTCTCGCTGGCTCAAAACACAGAGTGTGTCCATTTGGACAAACAGAGAG 302
 Db CCACTGCACTCTCGCTGGCTCAAAACACAGAGTGTGTCCATTTGGACAAACAGAGAG 373
 QY 303 GGAATTCAAAAGTATGGGCACTAG 327
 Db GGAATTCAAAAGTATGGGCACTAG 398

RESULT 9
 ADS09913/c
 ID ADS09913 standard; DNA; 3726 BP.
 XX
 AC ADS09913;
 AC
 DT 16-DEC-2004 (first entry)
 XX
 DE Human therapeutic DNA - SEQ ID 150.
 XX
 KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
 KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
 KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
 XX

ID ADQ92179 standard; DNA; 503 BP.
 AC ADQ92179;
 XX 07-OCT-2004 (first entry)
 DT Human autoantigen DNA fragment MPMGP800L05536.
 XX ds; autoantigen; antibody; hybridoma; biosensor chip;
 KW extracorporeal differential diagnosis; autoimmune disease;
 KW ribosomal protein; tubulin;
 KW dolichyl-diphospho-oligosaccharide-glycosyl transferase;
 KW multiple sclerosis; rheumatoid arthritis; epitope mapping;
 KW affinity chromatography; electrophoresis; autoantibody apheresis;
 KW RNA interference; RNAi.
 XX Homo sapiens.
 OS WO2004058972-A1.
 XX 15-JUL-2004.
 PD 23-DEC-2002; 2002WO-BP014731.
 XX 23-DEC-2002; 2002WO-BP014731.
 XX (THIE/) THIESEN H.
 PA (LORE/) LORENZ P.
 XX Thiesen H, Lorenz P;
 PI WPI; 2004-543459/52.
 XX New human DNA autoantigens, useful as assay, diagnostic, and prognostic
 DR reagents and for treating autoimmune disease, also related expression
 XX products and antibodies with similar uses.
 PT Claim 1; SEQ ID NO 160; 110pp; German.
 XX This invention describes novel human DNA autoantigens which are used to
 CC produce recombinant expression vectors; prokaryotic or eukaryotic cells;
 CC poly- or mono-clonal antibodies (Ab) specific; hybridomas that express
 CC monoclonal Ab; biosensor chips having an addressable sequence pattern as
 CC probes; medical or diagnostic instruments that include the biosensor; for
 CC extracorporeal differential diagnosis of autoimmune diseases and
 CC predisposition to them. The autoantigen polynucleotides encode ribosomal
 CC proteins; tubulins; dolichyl-diphospho-oligosaccharide-glycosyl
 CC transferases and proteins. The antibodies may be labelled conventionally
 CC with radioisotopes, coloured or fluorescent groups, or a member of the
 CC biotin/avidin pair, or colloidal gold. The autoantigens can be directed
 CC against mitochondria, liver-kidney microsomes; histidyl-tRNA; nuclear
 CC membrane; neutrophil/cytoplasm; insect cells; epidermal intracellular
 CC or basal membrane antigens; Golgi or cell nuclei, or associated with
 CC multiple sclerosis or rheumatoid arthritis. They are useful for epitope
 CC mapping; in affinity chromatography or electrophoresis; for diagnosis,
 CC prognosis, control of treatment or therapeutic response of autoimmune
 CC diseases, particularly in vitro differential diagnosis of autoimmune
 CC diseases; to produce biosensor chips or for autoantibody apheresis.
 CC Autoantigen DNA can be used for therapeutic RNA interference against
 CC autoantibodies. Biochips that carry the new materials are useful in
 CC medical and diagnostic instruments. ADQ92020-ADQ92280 represent human
 CC autoantigens.
 XX Sequence 503 BP; 131 A; 102 C; 120 G; 150 T; 0 U; 0 Other;
 SQ Query Match 97.9%; Score 320; DB 12; Length 503;
 Best Local Similarity 100.0%; Pred. NO. 1.1e-98;
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CAGCGATGGATGGATACCCGAGCGGACCAACAGCGCGCGGCAAGCGCTTTG 67
 DB 1 CAGCGATGGATGGATACCCGAGCGGACCAACAGCGCGCGGCAAGCGCTTTG 60

68 AAGTGAAGAAAGTGGAAATGAGTAGCCCTCTGGCCCTGGGATATTGTTGTAATACTGTG 127
 DB |||||
 61 AAGTGAAGAAAGTGGAAATGAGTAGCCCTCTGGCCCTGGGATATTGTTGTAATACTGTG 120
 QY |||||
 DB |||||
 128 CCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGAATGTCAAGCTAACCAAGGCGTCCG 187
 DB |||||
 121 CCATCTGCAGGAACCAACATTTATGGATCTTTGCATAGAATGTCAAGCTAACCAAGGCGTCCG 180
 QY |||||
 DB |||||
 188 CTACTTTCAAGAGAGTGTTACTGTGCGCATGGGAGTCTGTAACCATCTTTTCACTTCCACT 247
 DB |||||
 181 CTACTTTCAAGAGAGTGTTACTGTGCGCATGGGAGTCTGTAACCATCTTTTCACTTCCACT 240
 QY |||||
 DB |||||
 248 GCATCTCTCGTGGTCTAAAACACACAGAGTGTGTCATTTGGACAAACAGAGAGTGGGAAT 307
 DB |||||
 241 GCATCTCTCGTGGTCTAAAACACACAGAGTGTGTCATTTGGACAAACAGAGAGTGGGAAT 300
 QY |||||
 DB |||||
 308 TCCAAAAGTATGGGCACTAG 327
 DB |||||
 301 TCCAAAAGTATGGGCACTAG 320

RESULT 12
 ABV25615/c
 ID ABV25615 standard; cDNA; 4476 BP.
 XX AC
 AC ABV25615;
 XX DT
 DT 16-SEP-2002 (first entry)
 XX DE
 DE Human prostate expression marker cDNA 25606.
 XX KW
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene; ss.
 XX OS
 OS Homo sapiens.
 XX PN
 PN WO200160860-A2.
 XX PD
 PD 23-AUG-2001.
 XX PF
 PF 20-FEB-2001; 2001WO-US005171.
 XX PR
 PR 17-FEB-2000; 2000US-0183319P.
 PR 16-MAR-2000; 2000US-0189862P.
 PR 25-MAY-2000; 2000US-0207454P.
 PR 09-JUN-2000; 2000US-0211314P.
 PR 18-JUL-2000; 2000US-0219007P.
 PR 13-DEC-2000; 2000US-0255281P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX Schlegel R, Endege WO, Monahan JE;
 PI WPI; 2001-662795/76.
 DR Novel isolated nucleic acid molecule associated with cancerous state of
 PT prostate cells and correlating with presence of prostate cancer, useful
 PT for detecting presence of prostate cancer, stage of prostate cancer.
 XX Claim 1; Page 5119-5120; 11750pp; English.
 XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
 CC specification or its complement. (I) is useful for: (a) assessing whether
 CC a patient is afflicted with prostate cancer; (b) monitoring the
 CC progression of prostate cancer in a patient; (c) assessing the efficacy
 CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
 CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
 CC (e) selecting a composition for inhibiting prostate cancer in a patient;
 CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
 CC determining whether prostate cancer has metastasized in a patient; (h)
 CC assessing the aggressiveness or indolence of prostate cancer in a patient
 CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX Sequence 4476 BP; 1085 A; 1129 C; 1015 G; 1247 T; 0 U; 0 Other;
SQ Query Match 94.4%; Score 308.8; DB 5; Length 4476;
Best Local Similarity 99.4%; Pred. No. 2.2e-94;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 GCGCGCAGGATGGATGGATACCCGAGCGGACCAACAGCGCGCGGCAAGAGCG 62
DB 1018 GCCCGCAGCGATGGATGGATACCCGAGCGGACCAACAGCGCGCGGCAAGAGCG 959
QY 63 CTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 122
DB 958 CTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 899
QY 123 CTGTGCCATCTGCAGGAACCAATATGATGATCTTTGCATAGATCTCAAGCTTAACGAGC 182
DB 898 CTGTGCCATCTGCAGGAACCAATATGATGATCTTTGCATAGATCTCAAGCTTAACGAGC 839
QY 183 GTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTT 242
DB 838 GTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTT 779
QY 243 CCACTGCATCTCTCGCTCGCTCAAAACACAGCAGGTGTCTCATTTGGACACAGAGAGTG 302
DB 778 CCACTGCATCTCTCGCTCGCTCAAAACACAGCAGGTGTCTCATTTGGACACAGAGAGTG 719
QY 303 GGAATTCACAAA 314
DB 718 GGAATTCACAAA 707
RESULT 13
ID ABX39512 standard; cDNA; 380 BP.
XX AC ABX39512;
XX DT 20-FEB-2003 (first entry)
XX DE Bovine EST associated with lactation/muscle/fat deposition #4677.
XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX OS Bos Taurus.
XX PN US2002137139-A1.
XX XX 26-SEP-2002.
XX PF 24-SEP-2001; 2001US-00960352.
XX PR 12-JAN-1999; 99US-0115707P.
XX PR 11-JAN-2000; 2000US-00480902.
XX XX (BYAT/) BYATT J C.
XX PA (MATH/) MATHALAGAN N.
XX PA (TRON/) TRON N.
XX PA (WARR/) WARREN W C.
XX XX Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX DR New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.
XX PS Claim 2; SEQ ID NO 4677; 245pp; English.
XX CC The invention relates to a purified nucleic acid molecule associated with

CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non- translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
SQ Sequence 380 BP; 98 A; 87 C; 103 G; 92 T; 0 U; 0 Other;
Query Match 92.5%; Score 302.4; DB 8; Length 380;
Best Local Similarity 96.6%; Pred. No. 1e-92;
Matches 309; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
QY 8 CAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTTG 67
DB 2 CAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTTG 61
QY 68 AAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 127
DB 62 AAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 121
QY 128 CCATCTGCAGGAACCAACATATGATCTTTGCATAGATGTCAAGCTAACACGAGGCGCG 187
DB 122 CCATCTGCAGGAACCAACATATGATCTTTGCATAGATGTCAAGCTAACACGAGGCGCG 181
QY 188 CTACTTCTCAGAGAGTGTACTGTCTGCATGGGAGTCTGTAAACCATGCTTTTCACTTCCACT 247
DB 182 CTACTTCTCAGAGAGTGTACTGTCTGCATGGGAGTCTGTAAACCATGCTTTTCACTTCCACT 241
QY 248 GCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACAGAGAGTGGGAAT 307
DB 242 GCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACAGAGAGTGGGAAT 301
QY 308 TCCAAAAGTATGGGCACCTAG 327
DB 302 TCCAAAAGTATGGGCACCTAG 321
RESULT 14
ID AAS94844/C
ID AAS94844 standard; DNA; 5347 BP.
XX AC AAS94844;
XX XX 14-FEB-2002 (first entry)
XX DT Human DNA sequence #99 expressed during foam cell differentiation.
XX DE Human; foam cell differentiation; atherosclerosis; cerebral stroke;
KW cardiovascular disorder; coronary artery disease; gene therapy; ds.
XX XX Homo sapiens.
XX OS Homo sapiens.
XX PN WO200177389-A2.

XX 18-OCT-2001.
PD
XX
XX 04-APR-2001; 2001WO-US011128.
PF
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XX 05-APR-2000; 2000US-0195106P.
PR
XX
XX (INCY-) INCYTE GENOMICS INC.
PA
XX Shiffman D, Somogyi R, Lawn R, Seilhamer JJ, Porter GU, Mikita T;
PI Tai J;
XX
XX WPI; 2002-010925/01.
DR
XX
XX Composition useful for diagnosis of conditions, disorders or diseases
PT associated with atherosclerosis, comprises several polynucleotides that
PT are differentially expressed in foam cell development.
XX
XX Claim 1; Page 151-152; 315pp; English.
PS
XX The present invention relates to the isolation of human polynucleotide
CC sequences that are differentially expressed during foam cell
CC differentiation. The polynucleotide sequences of the invention or a
CC composition comprising these polynucleotides are useful as a high
CC throughput method for detecting altered expression of one or more
CC polynucleotides in a sample. The polynucleotides can be used in the
CC diagnosis of disorders associated with foam cell development such as
CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as
CC coronary artery disease. The polynucleotide sequences can also be used as
CC PCR primers and probes. The polynucleotides of the invention are also
CC useful in gene therapy. AAS94746-AAS95021 represent the human
CC polynucleotide sequences of the invention which are differentially
CC expressed during foam cell differentiation
XX
XX Sequence 5347 BP; 1489 A; 1277 C; 1094 G; 1487 T; 0 U; 0 Other;
SQ

Query Match 92.1%; Score 301.2; DB 6; Length 5347;
Best Local Similarity 98.7%; Pred. No. 9.4e-92;
Matches 314; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 3 GGCGGCGGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGGCGC-GGGCAAGAAGC 61
Db 519 GCCCGGCGGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGGCGGCGCAAGAAGC 460
QY 62 GCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTATA 121
Db 459 GCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGGCTGGGATATTGTGGTATA 400
QY 122 ACTGTGCCATCTGCAGGAACCAATATGGATCTTTGCATAGATGTCAAGCTAACCCAGG 181
Db 399 ACTGTGCCATCTGCAGGACCAATATGGATCTTTGCATAGATGTCAAGCTAACCCAGG 340
QY 182 CGTCCGCTACTTCAGAGAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTCACT 241
Db 339 CGTCCGCTACTTCAGAGAGTGTACTGTCCGATGGGAGTCTGTAAACCATGCTTTTCACT 280
QY 242 TCCACTGCATCTCTCGTGCTCTCAAAACAGACAGAGTGTCTTCATTTGGACACAGAGAGT 301
Db 279 TCCACTGCATCTCTCGTGCTCTCAAAACAGACAGAGTGTCTTCATTTGGACACAGAGAGT 220
QY 302 GGGAAATCCAAAGATATG 319
Db 219 GGGAAATCCAAAGATAGG 202

RESULT 15
ADF42703/C
ID ADF42703 standard; cDNA; 3484 BP.
XX
XX ADF42703;
AC
XX
DT 26-FEB-2004 (first entry)
XX

DE Human Testican-1 nucleotide sequence SEQ ID NO:9.
XX
XX diabetic; pre-diabetic; Type 2 diabetes; antidiabetic; gene therapy;
KW diabetes; insulin resistance; metabolic disease; human; gene; ss.
XX
XX Homo sapiens.
OS
XX WO2003102163-A2.
PN
XX 11-DEC-2003.
PD
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XX 04-JUN-2003; 2003WO-US017825.
PF
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XX 04-JUN-2002; 2002US-0385857P.
PR
XX 04-JUN-2002; 2002US-0386013P.
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XX 04-JUN-2002; 2002US-0386074P.
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XX 04-JUN-2002; 2002US-0386107P.
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XX 05-JUN-2002; 2002US-0386314P.
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XX 05-JUN-2002; 2002US-0386326P.
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XX 05-JUN-2002; 2002US-0386332P.
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XX 05-JUN-2002; 2002US-0386481P.
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XX 05-JUN-2002; 2002US-0386512P.
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XX 05-JUN-2002; 2002US-0386513P.
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XX 05-JUN-2002; 2002US-0386558P.
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XX 05-JUN-2002; 2002US-0386600P.
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XX 05-JUN-2002; 2002US-0386615P.
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XX 05-JUN-2002; 2002US-0386654P.
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XX 06-JUN-2002; 2002US-0386838P.
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XX 06-JUN-2002; 2002US-0386861P.
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XX 06-JUN-2002; 2002US-0386944P.
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XX 06-JUN-2002; 2002US-0386955P.
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XX 06-JUN-2002; 2002US-0387017P.
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XX 06-JUN-2002; 2002US-0387026P.
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XX 06-JUN-2002; 2002US-0387039P.
PR
XX 20-JUN-2002; 2002US-0386865P.
XX
XX (META-) METABOLEX INC.
PA
XX Allan B, Gregoire F, Lavan B, Moodie S, Waters S, Wong C;
PI
XX WPI; 2004-053469/05.
DR P-PSDB; ADF42704.
XX
XX Identifying an agent for treating diabetic or pre-diabetic individuals
PT comprises contacting an agent with a polypeptide, e.g., human ceramidase,
PT and selecting an agent that modulates the expression or activity of the
PT polypeptide.
XX
XX Disclosure; SEQ ID NO 9; 209pp; English.
PS
XX The present invention describes a method for identifying an agent for
CC treating a diabetic or pre-diabetic individual. The method comprises
CC contacting an agent to a mixture comprising a polypeptide encoded by a
CC nucleic acid that hybridises under stringent conditions to a nucleic acid
CC encoding any of the 23 fully defined amino acid sequences given in the
CC specification, and selecting an agent that modulates the expression or
CC activity of the polypeptide. Also described: (1) a method of treating a
CC diabetic or pre-diabetic animal, comprising administering to the animal a
CC therapeutic amount of an agent identified by the method described above;
CC (2) a method of introducing an expression cassette into a cell,
CC comprising introducing into the cell an expression cassette comprising a
CC promoter operably linked to a polynucleotide encoding a polypeptide,
CC where the polynucleotide hybridises under stringent conditions to a
CC nucleic acid encoding the above amino acid sequences; and (3) a method of
CC diagnosing an individual who has Type 2 diabetes or is pre-diabetic,
CC comprising detecting in a sample from the individual the level of a
CC polypeptide or the level of the above-mentioned polynucleotide encoding
CC the polypeptide, where a modulated level of the polypeptide or
CC polynucleotide in the sample compared to a level of the polypeptide or
CC polynucleotide in either a lean individual or a previous sample from the
CC individual indicates that the individual is diabetic or pre-diabetic. The
CC method is useful in diagnosing and treating diabetes, insulin resistance
CC or related metabolic diseases in human subjects. The method may also be

CC used in identifying agents for treating diabetic or pre-diabetic
CC individuals. The present sequence is used in the exemplification of the
CC present invention.

35X

SQ Sequence 3484 BP; 894 A; 910 C; 808 G; 872 T; 0 U; 0 Other;

Query Match 90.8%; Score 296.8; DB 12; Length 3484;

Query Match 50.0%; Score 250.0; SS 12; Length 3484
Best Local Similarity 99.3%; Pred. No. 2.4e-90;

Matches 298; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GGCGCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAGCG 62

Db 300 GCCCGCAGCGATGTGGATACCCCGAGCGGCCACACAGCGCGCGGGCAGAAGCG 241

QY 63 CTTGAAGTGAAAAAGTGGATGCAGTAGCCCTCTGGCCCTGGGATATTGTGGTTGATAA 122

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180
Db

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Db 120 GTCCGCTACTTCAGAAGAGTGTA CTGTCGATGGGAGTCTGTAA CCACTGCTTTTTCATT 61

Qy 243 CCACTGCATCTCTCGCTGCTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGAGTG 302

db 60 CCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACACAGAGGTG 1

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Job time : 365 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 24, 2005, 05:57:28 ; Search time 1566 Seconds
(without alignments)
1305.185 Million cell updates/sec

Title: US-09-541-462B-1

Perfect score: 327

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Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 6067389 seqs, 3125258755 residues

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

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- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	327	100.0	433	18	US-10-085-783A-43377
3	327	100.0	453	17	US-10-242-535A-35025
4	327	100.0	453	18	US-10-085-783A-35025
5	327	100.0	467	17	US-10-242-535A-39933
6	327	100.0	467	18	US-10-085-783A-39933
7	327	100.0	471	17	US-10-242-535A-57254

8	327	100.0	471	18	US-10-085-783A-57254	Sequence 57254, A
9	327	100.0	472	17	US-10-242-535A-56068	Sequence 56068, A
10	327	100.0	472	18	US-10-085-783A-56068	Sequence 56068, A
11	327	100.0	508	21	US-10-913-937-3	Sequence 3, Appli
12	327	100.0	523	17	US-10-242-535A-46292	Sequence 46292, A
13	327	100.0	523	18	US-10-085-783A-46292	Sequence 46292, A
14	325	99.4	476	10	US-09-918-995-17191	Sequence 17191, A
C 15	321.8	98.4	4543	14	US-10-198-846-11311	Sequence 11311, A
16	316	96.6	430	17	US-10-242-535A-54751	Sequence 54751, A
17	316	96.6	430	18	US-10-085-783A-54751	Sequence 54751, A
C 18	308.8	94.4	4476	20	US-10-357-930-25604	Sequence 25604, A
19	302.4	92.5	380	9	US-09-960-352-4677	Sequence 4677, Ap
C 20	301.2	92.1	5347	16	US-10-240-965-99	Sequence 99, Appl
C 21	296.8	90.8	3484	20	US-10-723-860-1383	Sequence 1383, Ap
C 22	296.8	90.8	5111	15	US-10-205-823-382	Sequence 382, App
C 23	296.8	90.8	5371	20	US-10-723-860-5852	Sequence 5852, Ap
C 24	290.2	88.7	504	21	US-10-913-937-5	Sequence 5, Appli
25	281	85.9	468	17	US-10-242-535A-47656	Sequence 47656, A
26	281	85.9	468	18	US-10-085-783A-47656	Sequence 47656, A
27	278.6	85.2	486	17	US-10-242-535A-52747	Sequence 52747, A
28	278.6	85.2	486	18	US-10-085-783A-52747	Sequence 52747, A
29	273.8	83.7	475	17	US-10-242-535A-50604	Sequence 50604, A
30	273.8	83.7	475	18	US-10-085-783A-50604	Sequence 50604, A
31	253.6	77.6	3208	9	US-09-780-016-27	Sequence 27, Appl
32	253.6	77.6	3208	14	US-10-214-811-27	Sequence 27, Appl
33	253.6	77.6	3208	19	US-10-766-074-27	Sequence 27, Appl
34	249	76.1	300	17	US-10-242-535A-48516	Sequence 48516, A
35	249	76.1	300	18	US-10-085-783A-48516	Sequence 48516, A
36	239	73.1	464	17	US-10-242-535A-58211	Sequence 58211, A
37	239	73.1	464	18	US-10-085-783A-58211	Sequence 58211, A
38	213.4	65.3	370	17	US-10-242-535A-19847	Sequence 19847, A
39	213.4	65.3	370	18	US-10-085-783A-19847	Sequence 19847, A
40	208.8	63.9	273	17	US-10-242-535A-46883	Sequence 46883, A
41	208.8	63.9	273	18	US-10-085-783A-46883	Sequence 46883, A
42	205.8	62.9	439	10	US-09-918-995-14771	Sequence 14771, A
C 43	191	58.4	1050	21	US-10-487-501-2521	Sequence 2521, Ap
C 44	191	58.4	1050	21	US-10-487-501-4357	Sequence 4357, Ap
C 45	190	58.1	608	19	US-10-767-795-687	Sequence 687, App

ALIGNMENTS

RESULT 1

US-10-242-535A-43377
; Sequence 43377, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43377
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-43377

Query Match 100.0%; Score 327; DB 17; Length 433;
Best Local Similarity 100.0%; Pred. No. 4,le-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGGCGAGCGATGGATGCGATACCCGAGCGGACCAACAGCGCGCGGCAAGAAG 60
 Db 20 ATGCGGCGAGCGATGGATGCGATACCCGAGCGGACCAACAGCGCGCGGCAAGAAG 79
 QY 61 CGCTTTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
 Db 80 CGCTTTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 139
 QY 121 AACTGTGCCATCTGCAAGGACCAATATGATGATCTTTGGATAGATGATCAAGCTAACCCAG 180
 Db 140 AACTGTGCCATCTGCAAGGACCAATATGATGATCTTTGGATAGATGATCAAGCTAACCCAG 199
 QY 181 GCGTCCGCTACTTCAAGAGAGTGTACTGCGCATGGGGAGTCTGTAAACCATGCTTTTCAC 240
 Db 200 GCGTCCGCTACTTCAAGAGAGTGTACTGCGCATGGGGAGTCTGTAAACCATGCTTTTCAC 259
 QY 241 TTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACACAGAG 300
 Db 260 TTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACACAGAG 319
 QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
 Db 320 TGGGAATTCAAAAGTATGGGCACTAG 346

RESULT 2
 US-10-085-783A-43377
 ; Sequence 43377, Application US/10085783A
 ; Publication No. US20040037841A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChondroGene Inc.
 ; APPLICANT: Liew, C.C.
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2002
 ; CURRENT APPLICATION NUMBER: US/10/085,783A
 ; CURRENT FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/305,340
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 58994
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 43377
 ; LENGTH: 433
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-085-783A-43377

Query Match 100.0%; Score 327; DB 18; Length 433;
 Best Local Similarity 100.0%; Pred. No. 4.1e-104;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCGGCGAGCGATGGATGCGATACCCGAGCGGACCAACAGCGCGCGGCAAGAAG 60
 Db 20 ATGCGGCGAGCGATGGATGCGATACCCGAGCGGACCAACAGCGCGCGGCAAGAAG 79
 QY 61 CGCTTTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
 Db 80 CGCTTTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 139
 QY 121 AACTGTGCCATCTGCAAGGACCAATATGATGATCTTTGGATAGATGATCAAGCTAACCCAG 180
 Db 140 AACTGTGCCATCTGCAAGGACCAATATGATGATCTTTGGATAGATGATCAAGCTAACCCAG 199
 QY 181 GCGTCCGCTACTTCAAGAGAGTGTACTGCGCATGGGGAGTCTGTAAACCATGCTTTTCAC 240
 Db 200 GCGTCCGCTACTTCAAGAGAGTGTACTGCGCATGGGGAGTCTGTAAACCATGCTTTTCAC 259
 QY 241 TTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACACAGAG 300

Db 260 TTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACACAGAG 319
 QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
 Db 320 TGGGAATTCAAAAGTATGGGCACTAG 346
 RESULT 3
 US-10-242-535A-35025
 ; Sequence 35025, Application US/10242535A
 ; Publication No. US20040013663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChondroGene Inc.
 ; APPLICANT: Liew, C.C.
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2005
 ; CURRENT APPLICATION NUMBER: US/10/242,535A
 ; CURRENT FILING DATE: 2002-09-12
 ; PRIOR APPLICATION NUMBER: US 10/085,783
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/305,340
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/275,017
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 60/271,955
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 58994
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 35025
 ; LENGTH: 453
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-242-535A-35025

Query Match 100.0%; Score 327; DB 17; Length 453;
 Best Local Similarity 100.0%; Pred. No. 4.2e-104;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGCGGCGAGCGATGGATGCGATACCCGAGCGGACCAACAGCGCGCGGCAAGAAG 60
 Db 24 ATGCGGCGAGCGATGGATGCGATACCCGAGCGGACCAACAGCGCGCGGCAAGAAG 83
 QY 61 CGCTTTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
 Db 84 CGCTTTGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 143
 QY 121 AACTGTGCCATCTGCAAGGACCAATATGATGATCTTTGGATAGATGATCAAGCTAACCCAG 180
 Db 144 AACTGTGCCATCTGCAAGGACCAATATGATGATCTTTGGATAGATGATCAAGCTAACCCAG 203
 QY 181 GCGTCCGCTACTTCAAGAGAGTGTACTGCGCATGGGGAGTCTGTAAACCATGCTTTTCAC 240
 Db 204 GCGTCCGCTACTTCAAGAGAGTGTACTGCGCATGGGGAGTCTGTAAACCATGCTTTTCAC 263
 QY 241 TTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACACAGAG 300
 Db 264 TTCCACTGTCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACACAGAG 323
 QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
 Db 324 TGGGAATTCAAAAGTATGGGCACTAG 350

RESULT 4
 US-10-085-783A-35025
 ; Sequence 35025, Application US/10085783A
 ; Publication No. US20040037841A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChondroGene Inc.
 ; APPLICANT: Liew, C.C.
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2002
 ; CURRENT APPLICATION NUMBER: US/10/085,783A

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; CURRENT FILLING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILLING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILLING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILLING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35025
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-35025

Query Match      100.0%; Score 327; DB 18; Length 453;
Best Local Similarity 100.0%; Pred. No. 4.2e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
DB 84 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 143
QY 121 AACTGTGCCATCTCGAGGAACCAATATGATCTTTGCATAGATGTCAAGCTAACCCAG 180
DB 144 AACTGTGCCATCTCGAGGAACCAATATGATCTTTGCATAGATGTCAAGCTAACCCAG 203
QY 181 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACCATGCTTTTTCAC 240
DB 204 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACCATGCTTTTTCAC 263
QY 241 TTCACCTGCATCTCGCTGGCTCAAAACACAGCAGGTGTCTCCATTGGACAACAGAGAG 300
DB 264 TTCACCTGCATCTCGCTGGCTCAAAACACAGCAGGTGTCTCCATTGGACAACAGAGAG 323
QY 301 TGGGAATTCCTCAAAAGTATGGGCACTAG 327
DB 324 TGGGAATTCCTCAAAAGTATGGGCACTAG 350

RESULT 5
US-10-242-535A-39933
; Sequence 39933, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILLING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILLING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILLING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILLING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILLING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39933
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-39933

Query Match      100.0%; Score 327; DB 17; Length 467;
Best Local Similarity 100.0%; Pred. No. 4.2e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
DB 24 ATGGCGGAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 83
QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
DB 84 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 143
QY 121 AACTGTGCCATCTCGAGGAACCAATATGATCTTTGCATAGATGTCAAGCTAACCCAG 180
DB 144 AACTGTGCCATCTCGAGGAACCAATATGATCTTTGCATAGATGTCAAGCTAACCCAG 203
QY 181 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACCATGCTTTTTCAC 240
DB 204 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACCATGCTTTTTCAC 263
QY 241 TTCACCTGCATCTCGCTGGCTCAAAACACAGCAGGTGTCTCCATTGGACAACAGAGAG 300
DB 264 TTCACCTGCATCTCGCTGGCTCAAAACACAGCAGGTGTCTCCATTGGACAACAGAGAG 323
QY 301 TGGGAATTCCTCAAAAGTATGGGCACTAG 327
DB 324 TGGGAATTCCTCAAAAGTATGGGCACTAG 350

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US-10-085-783A-39933
; Sequence 39933, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILLING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILLING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILLING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILLING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39933
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-39933

Query Match      100.0%; Score 327; DB 18; Length 467;
Best Local Similarity 100.0%; Pred. No. 4.2e-104;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
DB 20 ATGGCGGAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 79
QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
DB 80 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 139
QY 121 AACTGTGCCATCTCGAGGAACCAATATGATCTTTGCATAGATGTCAAGCTAACCCAG 180
DB 140 AACTGTGCCATCTCGAGGAACCAATATGATCTTTGCATAGATGTCAAGCTAACCCAG 199
QY 181 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACCATGCTTTTTCAC 240
DB 200 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAACCATGCTTTTTCAC 259
QY 241 TTCACCTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTCTCCATTGGACAACAGAGAG 300
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OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (455)..(455)
 OTHER INFORMATION: n is a, c, g, or t
 US-10-242-535A-56068

Query Match
 Best Local Similarity 100.0%; Score 327; DB 17; Length 472;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAG 60
 DB 20 ATGGCGGAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAG 79
 QY 61 CGCTTTGAAGTGAAAAGTGGAAATGCAATGAGTGGGCTCTGGGCTGGGATATTGTTGAT 120
 DB 80 CGCTTTGAAGTGAAAAGTGGAAATGCAATGAGTGGGCTCTGGGCTGGGATATTGTTGAT 139
 QY 121 AACTGTGCCATCTCGAGAACCAACATATTGATCTTTGCATAGAAATGCTCAAGCTAACCCAG 180
 DB 140 AACTGTGCCATCTCGAGAACCAACATATTGATCTTTGCATAGAAATGCTCAAGCTAACCCAG 199
 QY 181 GGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTGTGTCAAGCTAACCCAG 240
 DB 200 GGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTGTGTCAAGCTAACCCAG 259
 QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGAGTGTGTCCATTTGGACAAACAGAGAG 300
 DB 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGAGTGTGTCCATTTGGACAAACAGAGAG 319
 QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
 DB 320 TGGGAATTCAAAAGTATGGGCACTAG 346

RESULT 10
 US-10-085-783A-56068
 ; Sequence 56068, Application US/10085783A
 ; Publication No. US20040037841A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChondroGene Inc.
 ; APPLICANT: Liaw, C.C.
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2002
 ; CURRENT APPLICATION NUMBER: US/10/085,783A
 ; CURRENT FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/305,340
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/275,017
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 60/271,955
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 58994
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 56068
 ; LENGTH: 472
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (437)..(437)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (455)..(455)
 OTHER INFORMATION: n is a, c, g, or t
 US-10-085-783A-56068

Query Match
 Best Local Similarity 100.0%; Score 327; DB 18; Length 472;
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAG 60
 DB 20 ATGGCGGAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAG 79
 QY 61 CGCTTTGAAGTGAAAAGTGGAAATGCAATGAGTGGGCTCTGGGCTGGGATATTGTTGAT 120
 DB 80 CGCTTTGAAGTGAAAAGTGGAAATGCAATGAGTGGGCTCTGGGCTGGGATATTGTTGAT 139
 QY 121 AACTGTGCCATCTCGAGAACCAACATATTGATCTTTGCATAGAAATGCTCAAGCTAACCCAG 180
 DB 140 AACTGTGCCATCTCGAGAACCAACATATTGATCTTTGCATAGAAATGCTCAAGCTAACCCAG 199
 QY 181 GGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTGTGTCAAGCTAACCCAG 240
 DB 200 GGTCCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTGTGTCAAGCTAACCCAG 259
 QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGAGTGTGTCCATTTGGACAAACAGAGAG 300
 DB 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGAGTGTGTCCATTTGGACAAACAGAGAG 319
 QY 301 TGGGAATTCAAAAGTATGGGCACTAG 327
 DB 320 TGGGAATTCAAAAGTATGGGCACTAG 346

RESULT 11
 US-10-913-937-3
 ; Sequence 3, Application US/10913937
 ; Publication No. US20050019813A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Conaway, Joan A.
 ; APPLICANT: Conaway, Ronald C.
 ; APPLICANT: Kamura, Takumi
 ; APPLICANT: Orlanoma Medical Research Foundation
 ; TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor
 ; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
 ; FILE REFERENCE: 021044-004600US
 ; CURRENT APPLICATION NUMBER: US/10/913,937
 ; CURRENT FILING DATE: 2004-08-05
 ; PRIOR APPLICATION NUMBER: US/09/914,324
 ; PRIOR FILING DATE: 2001-08-22
 ; PRIOR APPLICATION NUMBER: US 60/121,787
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
 ; PRIOR FILING DATE: 2000-02-25
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 508
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
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 LOCATION: (7)..(333)
 OTHER INFORMATION: Rbx1
 US-10-913-937-3

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 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAG 60
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 QY 61 CGCTTTGAAGTGAAAAGTGGAAATGCAATGAGTGGGCTCTGGGCTGGGATATTGTTGAT 120
 DB 67 CGCTTTGAAGTGAAAAGTGGAAATGCAATGAGTGGGCTCTGGGCTGGGATATTGTTGAT 126
 QY 121 AACTGTGCCATCTCGAGAACCAACATATTGATCTTTGCATAGAAATGCTCAAGCTAACCCAG 180
 DB 127 AACTGTGCCATCTCGAGAACCAACATATTGATCTTTGCATAGAAATGCTCAAGCTAACCCAG 186

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 24, 2005, 00:30:07 ; Search time 2179 Seconds
(without alignments)
5712.261 Million cell updates/sec

Title: US-09-541-462B-1

Perfect score: 327

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hlc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	462	7 CN305890	170005830
2	327	100.0	471	4 BG339057	602436882
3	327	100.0	473	5 BX283972	602436882
4	327	100.0	488	4 BG777485	602664820
5	327	100.0	498	6 CB296618	12822005
6	327	100.0	509	7 CN305892	170006001
7	327	100.0	522	1 AL711573	DKFp6861
8	327	100.0	525	4 BG337472	602435003
9	327	100.0	527	4 BM715215	UI-B-CL1
10	327	100.0	527	5 BU932751	AGENCOURT
11	327	100.0	527	6 CB999822	AGENCOURT
12	327	100.0	529	4 BM757406	K-EST0036
13	327	100.0	531	6 CD523457	AGENCOURT
14	327	100.0	533	5 BU729963	UI-B-CK1
15	327	100.0	537	4 BG478622	60252509
16	327	100.0	545	5 BU941262	AGENCOURT
17	327	100.0	546	4 BI198015	602762132
18	327	100.0	546	5 BU601181	AGENCOURT
19	327	100.0	548	1 AV716338	AV716338
20	327	100.0	548	5 BU601301	AGENCOURT
21	327	100.0	549	4 BI958425	603386437
22	327	100.0	550	5 BU955646	AGENCOURT
23	327	100.0	554	6 CD249363	AGENCOURT
24	327	100.0	555	5 BU532840	AGENCOURT

25	327	100.0	555	5 BU601080	AGENCOURT
26	327	100.0	557	5 BU954591	AGENCOURT
27	327	100.0	558	6 CD388268	AGENCOURT
28	327	100.0	559	7 CK003869	AGENCOURT
29	327	100.0	562	6 CD175085	AGENCOURT
30	327	100.0	563	5 BU861191	AGENCOURT
31	327	100.0	570	5 BU597842	AGENCOURT
32	327	100.0	573	5 BU533405	AGENCOURT
33	327	100.0	581	5 BF308845	BP308845
34	327	100.0	583	5 BF317451	BP317451
35	327	100.0	616	4 BG705958	602669278
36	327	100.0	736	4 BG503311	602550721
37	327	100.0	801	5 BU533420	AGENCOURT
38	327	100.0	845	5 BU59349	AGENCOURT
39	327	100.0	886	4 BG481544	602528456
40	327	100.0	904	4 BM459634	AGENCOURT
41	327	100.0	945	5 BQ216738	AGENCOURT
42	327	100.0	1098	5 BQ050461	AGENCOURT
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ALIGNMENTS

RESULT 1
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LOCUS 17000583044616 GRN_PREHEP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN305890
VERSION CN305890.1 GI:47322304
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 462)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R., Lebkowski, J. and Stanton, L. W.
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 462 Std Error: 0.00.

FEATURES

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/db_xref="taxon:9606"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.3e-91;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGGCGGCGAGCGATGTGATATCCCGAGCGCACCACAGCGCGCGGCAAGAG 60
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Db 23 ATGGCGGCGAGCGATGTGATATCCCGAGCGCACCACAGCGCGCGGCGCAAGAG 82
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QY 61 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGTGGTTGAT 120
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QY 121 AACTGTGCCATCTGCAGGAAACCAATATATGATCTTTGGCATAGATGTCAAGCTAACACAG 180
DB 143 AACTGTGCCATCTGCAGGAAACCAATATATGATCTTTGGCATAGATGTCAAGCTAACACAG 202
QY 181 GCGTCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
DB 203 GCGTCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 262
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCATTTGGACAACACAGAG 300
DB 263 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCATTTGGACAACACAGAG 322
QY 301 TGGGAATTCAAAAGTATGGCACTAG 327
DB 323 TGGGAATTCAAAAGTATGGCACTAG 349

RESULT 2
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LOCUS 602436882F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4554597 5',
DEFINITION mRNA sequence.
ACCESSION BG339057
VERSION BG339057.1 GI:13145495
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 471)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: sgapps@email.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LICM1254 row: d column: 22
High quality sequence stop: 470.
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/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_46"
/notes="Organ: uterus; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
ORIGIN
Query Match 100.0%; Score 327; DB 4; Length 471;
Best Local Similarity 100.0%; Pred. No. 3.3e-91;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCGGACGCGATGTGATGTGATATACCCGAGCGGACCAACAGCGCGCGGCAAGAAG 60

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DB 42 ATGGCGGACGCGATGTGATGTGATATACCCGAGCGGACCAACAGCGCGCGGCAAGAAG 101
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DB 102 CGCTTTGAAGTGAAGTGAATGCAGTAGCCCTCTGGCCCTGGGATATTGTGGTTGAT 161
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DB 162 AACTGTGCCATCTGCAGGAAACCAATATATGATCTTTGGCATAGATGTCAAGCTAACACAG 221
QY 181 GCGTCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
DB 222 GCGTCGCTACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 281
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCATTTGGACAACACAGAG 300
DB 282 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCATTTGGACAACACAGAG 341
QY 301 TGGGAATTCAAAAGTATGGCACTAG 327
DB 342 TGGGAATTCAAAAGTATGGCACTAG 368

RESULT 3
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LOCUS 602436882F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:958P131435 ;
DEFINITION IMAGE:4652028, mRNA sequence.
ACCESSION BG339057
VERSION BG339057.1 GI:28848426
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 473)
AUTHORS Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,
Radelof, U., Schneider, D. and Korn, B.
TITLE Human Unigeneset - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD: IWAGp958P131435.
RZPDLIB: I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
PCMW-M13u, Primer sequence: CGTTGTAACACGACGCCACT.
FEATURES
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/db_xref="taxon:9606"
/clone="IMAGE:958P131435 ; IMAGE:4652028"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/notes="Organ: placenta; Vector: pOTB7; Site:1: XhoI;
Site:2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit

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3' adaptor sequence:
5'-ATTTAGAGGCGAGGGCGGCACATG-dT(30)BN-3' (where B = A, C, G or T). Average insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."

BN-3, 6

kb (range 0.9–4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."

els

CGGGCGCGG
|||||
CGGGCGCGG

GGGATATT
|||||
GGGATATT

ATGTCAAA
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TAACCAT
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TAACCAT

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1000

ear E
library
2.ab1 5

logY

X"

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/Clone_lib="Chimpanzee brain library Roos"
/notes="Vector: pUCH1; Site 1: Sfil-A; Site 2: Sfil-B; The
library was prepared using the SMART cDNA library
construction kit (Clontech), doing only primer extension,
but not PCR amplification of the cDNA. The only deviation
from the published protocol was that we cloned the cDNA
into a plasmid vector."

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ORIGIN	Query Match	100.0%;	Score 327;	DB 6;	Length 498;
	Best Local Similarity	100.0%;	Pred. No. 3.4e-91;		
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QY	61	CGCTTTGAAGTGA AAAAGTGGAAATGTCAGTAGCCCTCTGGGCGCTGGGATATTGTGGTTGAT	120		
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QY	121	AACGTGTGCCATCTGCAGGAAACCAATTATTGGATCTTTGCATPAGAAATGTCAAAGCTAAACGAG	180		
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QY	241	TTCCACTGTGCATCTCTCGCTGGCTCAAAAACACGACAGGAGTGTGTCCATTGGCAACACAGAGAG	300		
DB	242	TTCCACTGTGCATCTCTCGCTGGCTCAAAAACACGACAGGAGTGTGTCCATTGGCAACACAGAGAG	301		
QY	301	TGGGAATTCCAAAAGTATGGGCACCTAG	327		
DB	302	TGGGAATTCCAAAAGTATGGGCACCTAG	328		

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RESULT 6
LOCUS      CN305892
DEFINITION 17000600185586 GRN_PRENEU Homo sapiens cDNA 5', mRNA sequence.
ACCESSION  CN305892
VERSION     CN305892.1  GI:47322306
KEYWORDS   EST.
SOURCE      Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1  (bases 1 to 509)
AUTHORS    Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J.,
            Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M. S., Mandalam, R.,
            Lebkowski, J and Stanton, L.W.
TITLE       Transcriptionome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
JOURNAL     Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
            Regenerative Medicine
            Genon Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8658
            Fax: 650 473 7760
            Email: rbrandenberger@genon.com
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of all-trans retinoic and mitogens."
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ORIGIN

Query Match	100.0%;	Score 327;	DB 7;	Length 509;
Best Local Similarity	100.0%;	Pred. No. 3.4e-91;		
Matches 327;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Qy	181	GCCTCCGCTACTTCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC	240	
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Qy	301	TGGGAATTCAAAAGTATGGGCACTAG	327	
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RESULT 7

AL7111573	AL7111573	522 bp	mRNA	linear	EST 04-SEP-2003
LOCUS	DFK2P68G10483.r1.686 (synonym: hlcc3)			Homo sapiens cDNA clone	
DEFINITION	DFK2P68G10483.5', mRNA sequence.				
ACCESSION	AL7111573				
VERSION	AL7111573.1	GI:19694928			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 522)				
AUTHORS	Koehler,K., Beyer,A., Mewes,W., Weil,B. and Wiemann,S.				
TITLE	EST (Koehler,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S.)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: MIPS				
	WIPSC				

MLPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sponsored by BMFZ (Biomedical Research Center at the Charité,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.

NO sl sequence available.
This clone (DKZP68610483) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg. GRFMAN: Email: clone@rzpd.de.

FEATURES
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/clone.lib="686 (synonym: hicc3)"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN
Query Match      100.0%; Score 327; DB 1; Length 522;
Best Local Similarity 100.0%; Pred. No. 3.4e-91;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGAGCATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
DB 21 ATGGCGGCGAGCATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 80
QY 61 CGCTTTGAAGTCAAAAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGTTGAT 120
DB 81 CGCTTTGAAGTCAAAAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGTTGAT 140
QY 121 AACTGTGCCATCTGCAGGAACACATATTGATCTTTGCATAGATGTCAAGCTAACACAG 180
DB 141 AACTGTGCCATCTGCAGGAACACATATTGATCTTTGCATAGATGTCAAGCTAACACAG 200
QY 181 GCGTCGGCTACTTCAGAGAGTGTACTGTGCATGGGAGTCTGTAAACATGCTTTTCAC 240
DB 201 GCGTCGGCTACTTCAGAGAGTGTACTGTGCATGGGAGTCTGTAAACATGCTTTTCAC 260
QY 241 TTCCTACTGCATCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACAACAGAGAG 300
DB 261 TTCCTACTGCATCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACAACAGAGAG 320
QY 301 TGGGAATTCCAAAGTATGGGCACCTAG 327
DB 321 TGGGAATTCCAAAGTATGGGCACCTAG 347

RESULT 8
BG337472
LOCUS 602435003F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4553064 5',
DEFINITION mRNA sequence.
ACCESSION BG337472
VERSION BG337472.1 GI:13143910
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM1250 row: e column: 01
High quality sequence stop: 525.
Location/Qualifiers
1..525
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4553064"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 46"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:

```

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GGCAGGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match      100.0%; Score 327; DB 4; Length 525;
Best Local Similarity 100.0%; Pred. No. 3.4e-91;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGCGAGCATGGATGGATACCCCGAGCGGCACCAACAGCGCGGCAAGAAG 60
DB 7 ATGGCGGCGAGCATGGATGGATACCCCGAGCGGCACCAACAGCGCGGCAAGAAG 66
QY 61 CGCTTTGAAGTCAAAAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGTTGAT 120
DB 67 CGCTTTGAAGTCAAAAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGTTGAT 126
QY 121 AACTGTGCCATCTGCAGGAACACATATTGATCTTTGCATAGATGTCAAGCTAACACAG 180
DB 127 AACTGTGCCATCTGCAGGAACACATATTGATCTTTGCATAGATGTCAAGCTAACACAG 186
QY 181 GCGTCGGCTACTTCAGAGAGTGTACTGTGCATGGGAGTCTGTAAACATGCTTTTCAC 240
DB 187 GCGTCGGCTACTTCAGAGAGTGTACTGTGCATGGGAGTCTGTAAACATGCTTTTCAC 246
QY 241 TTCCTACTGCATCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACAACAGAGAG 300
DB 247 TTCCTACTGCATCTCGCTGGCTCAAAACACAGCAGGTGTGTCCATTGGACAACAGAGAG 306
QY 301 TGGGAATTCCAAAGTATGGGCACCTAG 327
DB 307 TGGGAATTCCAAAGTATGGGCACCTAG 333

RESULT 9
BG715215
LOCUS UI-E-CL1-afi-h-19-0-UI-r2 UI-E-CL1 Homo sapiens cDNA clone
DEFINITION UI-E-CL1-afi-h-19-0-UI 5', mRNA sequence.
ACCESSION BG715215
VERSION BG715215.1 GI:19028473
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
TITLE Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalizaiton and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Reverse.
Location/Qualifiers
1..527
/organism="Homo sapiens"

```

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-Cl1-afi-h-19-0-UI"
/tissue_type="human retina"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-Cl1"
/note="Organ: eye; Vector: p7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-Cl1 is a normalized cDNA library containing the
following tissue(s): retina. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into p7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CCGCG. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI)."
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ORIGIN

```
Query Match      100.0%; Score 327; DB 4; Length 527;
Best Local Similarity 100.0%; Pred. No. 3.4e-91;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
   |||||||
DB 4 ATGGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 63

QY 61 CGCTTTGAAGTGAAGAGTGGATGAGTACCGCTCTGGGCCTGGGATATTGTGGTTGAT 120
   |||||||
DB 64 CGCTTTGAAGTGAAGAGTGGATGAGTACCGCTCTGGGCCTGGGATATTGTGGTTGAT 123

QY 121 AACTGTGCCATCTGCAGAACCAACATTATGATGATCTTTGGCATAGATGTCAGCTAACCCAG 180
   |||||||
DB 124 AACTGTGCCATCTGCAGAACCAACATTATGATGATCTTTGGCATAGATGTCAGCTAACCCAG 183

QY 181 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGATGGGGAGTGTGTAAACCATGCTTTTTCAC 240
   |||||||
DB 184 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGATGGGGAGTGTGTAAACCATGCTTTTTCAC 243

QY 241 TTCCACTGCACTCTCGCTCGCTCAAAACAGCAGCGTGTGTCATTGGACACACAGAG 300
   |||||||
DB 244 TTCCACTGCACTCTCGCTCGCTCAAAACAGCAGCGTGTGTCATTGGACACACAGAG 303

QY 301 TGGGAATTCCAAAGTATGGGCACTAG 327
   |||||||
DB 304 TGGGAATTCCAAAGTATGGGCACTAG 330
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RESULT 10
BU932751      527 bp mRNA linear EST 18-OCT-2002
LOCUS
DEFINITION AGENCOURT 10473929 NIH_MGC_127 Homo sapiens cDNA clone
IMAGE:6673337 5', mRNA sequence.
ACCESSION BU932751
VERSION BU932751.1 GI:24121570
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 527)
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
```

```
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM2955 row: e column: 17
High quality sequence stop: 498.
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FEATURES

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source
1..527
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6673337"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_127"
/note="Vector: pDNK-LiB; Site 1: SfiI (ggccattatggcc);
Site 2: SfiI (ggcccttcggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -
5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,
salivary gland - 1.3%, and skin - 2.3%). 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAGCAGAGTGGCATTCGCGCGG-3' and
5'-ATCTAGGCGCGGCGCGGCGGACATG-3' (30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 1-2 kb
size fraction (other fractions present in NIH MGC 126 and
NIH MGC 128). Library created in the laboratory of T.
Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC
Library."
```

ORIGIN

```
Query Match      100.0%; Score 327; DB 5; Length 527;
Best Local Similarity 100.0%; Pred. No. 3.4e-91;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGGCAAGAAG 60
   |||||||
DB 24 ATGGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGGCAAGAAG 83

QY 61 CGCTTTGAAGTGAAGAGTGGATGAGTACCGCTCTGGGCCTGGGATATTGTGGTTGAT 120
   |||||||
DB 84 CGCTTTGAAGTGAAGAGTGGATGAGTACCGCTCTGGGCCTGGGATATTGTGGTTGAT 143

QY 121 AACTGTGCCATCTGCAGAACCAACATTATGATGATCTTTGGCATAGATGTCAGCTAACCCAG 180
   |||||||
DB 144 AACTGTGCCATCTGCAGAACCAACATTATGATGATCTTTGGCATAGATGTCAGCTAACCCAG 203

QY 181 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGATGGGGAGTGTGTAAACCATGCTTTTTCAC 240
   |||||||
DB 204 GCGTCCGCTACTTCAGAAAGTGTACTGTGCGATGGGGAGTGTGTAAACCATGCTTTTTCAC 263

QY 241 TTCCACTGCACTCTCGCTCGCTCAAAACAGCAGCGTGTGTCATTGGACACACAGAG 300
   |||||||
DB 264 TTCCACTGCACTCTCGCTCGCTCAAAACAGCAGCGTGTGTCATTGGACACACAGAG 323

QY 301 TGGGAATTCCAAAGTATGGGCACTAG 327
   |||||||
DB 324 TGGGAATTCCAAAGTATGGGCACTAG 350
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```
RESULT 11
CB999822
LOCUS
DEFINITION AGENCOURT 13645988 NIH_MGC_186 Homo sapiens cDNA clone
IMAGE:30322649 5', mRNA sequence.
ACCESSION CB999822
VERSION CB999822.1 GI:30294342
KEYWORDS EST.
SOURCE Homo sapiens (human)
```

ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 527) NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-x@mail.nih.gov Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov Plate: NDCM123 row: p column: 18 High quality sequence spot: 518.
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

FEATURES

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1. 527
location/qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IWAGE:30322649"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_186"
/notes="Organ: Pooled-Skin; Vector: pDNR-LTB; Site 1: SfiI
(ggcctatggccc); Site 2: SfiI (ggcgcctccggcc); library is
oligo-dT primed and directionally cloned. cDNA was
prepared from a pooled samples of tissues from Skin,
meninges, duramatter, pia matter and choroid plexus.
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATATGCG-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGGCCGACATG-AT(30)EN-3'
(where B = A, C, G and N = A, C, G, or T). Average
insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library"

```

ORIGIN

Query Match 100.0%; Score 327; DB 6; Length 527;
Best Local Similarity 100.0%; Pred. No. 3.4e-91;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1	ATGCGCGCAGCGATGTGGATATCCCGCGCGGCGACCAACAGCGCGCGCGGCGCAAGAG	60	Qy
25	ATGCGCGCAGCGATGTGGATATCCCGCGCGGCGACCAACAGCGCGCGCGGCGCAAGAG	84	Db
61	CGCTTTGAAGTGAAGAGTGGAAATGCGAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT	120	Qy
85	CGCTTTGAAGTGAAGAGTGGAAATGCGAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT	144	Db
121	AACGTGCGCATCTGCAGGAACCAATTATGATCTTTTGCATAGAATGTCAGACTAACCCAG	180	Qy
145	AACGTGCGCATCTGCAGGAACCAATTATGATCTTTTGCATAGAATGTCAGACTAACCCAG	204	Db
181	GGTCCGCTACTTCAGAAAGTGTACTGTCCGATGGGGAGTCTGTAAACCATGCTTTTTCAC	240	Qy
205	GGTCCGCTACTTCAGAAAGTGTACTGTCCGATGGGGAGTCTGTAAACCATGCTTTTTCAC	264	Db
241	TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACCAACAGAGAG	300	Qy
265	TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACCAACAGAGAG	324	Db
301	TGGGAATTCGAAAGTATGGGCACATAG	327	Qy
325	TGGGAATTCGAAAGTATGGGCACATAG	351	Db

RESULT 12
BM757406

LOCUS	BM757406	529 bp	mRNA	linear	EST 04-MAR-2002
DEFINITION	K-EST0036388 SISNUS Homo sapiens cDNA clone S1SNUS-29-H12 5', mRNA sequence.				
ACCESSION	BM757406				
VERSION	BM757406.1				
KEYWORDS	EST.				
SOURCE	GI:19087021				
ORGANISM	Homo sapiens (human)				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 529)				
AUTHORS	Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.				
TITLE	21C Frontier Korean EST Project 2001				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Kim YS Genome Research Center Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 29 row: H column: 12 High quality sequence stop: 529.				

FEATURES

```

1. 529
location/qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cdname="S1SNUS-29-H12"
/sex="F"
/tissue_type="Lymphoblast"
/cell_type="Lymphoblast-like"
/cell_line="SNU-5"
/lab_host="Top10F"
/clone_lib="S1SNUS"
/notes="Organ: Stomach; Vector: Site 2; NotI; The poly (A)+ R bacterial alkaline phosphatase with tabacco acid pyrophosphatase with intact mRNA was ligated with intact mRNA was ligated with I site by treatment of T4 RNAse. cDNA was synthesized from oligo priming with dr-tailed vector, adjusted to have about 60nt. circularized with E. coli DNALinker, EcoRI which site is also incl. converted to a DNA strand by obtained cDNA vectors were used. component cells E. coli Top10. The cDNA libraries constructed. full-length enriched cDNA lib

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ORIGIN

	Query Match	100.0%;	Score 327;	DB 4;	Length 529;
	Best Local Similarity	100.0%;	Pred. No. 3.4e-91;		
	Matches 327;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGCGGCGCAGCATGGATGTGGATACCCGAGCGGCCAACACAGCGCGCGGCCGAAGAAG	60		
Db	33	ATGCGGCGCAGCATGGATGTGGATACCCGAGCGGCCAACACAGCGCGCGGCCGAAGAAG	92		
QY	61	CGCTTTTGAAGTGAAGTGAAGTGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTTGAT	120		
Db	93	CGCTTTTGAAGTGAAGTGAAGTGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTTGAT	152		
QY	121	AACGTGGCCATCTGCAGGAAACACATATTGGAATCTTTTGCATAGAATGTCAGGCTAACCCAG	180		
Db	153	AACGTGGCCATCTGCAGGAAACACATATTGGAATCTTTTGCATAGAATGTCAGGCTAACCCAG	212		
QY	181	GGGTCCGCTACTTTCAGAAAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTTCAC	240		

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Db      213 GCGTCGCTACTTTCAGAGAGTGTACTGTGCGATGGGGAGTCTGTAAACCATGCTTTTCAC 1272
Qy      241 TTCCACTGATCTCTCGCTGGTCAAAACACGACAGGTGTGTCCTATGGACACAGAGAG 300
Db      273 TTCCACTGATCTCTCGCTGGTCAAAACACGACAGGTGTGTCCTATGGACACAGAGAG 332
Qy      301 TGGGAATTCAAAAGTATGGCACTAG 327
Db      333 TGGGAATTCAAAAGTATGGCACTAG 359

RESULT 13
CD523457
LOCUS   CD523457
DEFINITION AGENCOURT_14360071 NIH_MGC_191 Homo sapiens cDNA clone
IMAGE:30412182 5', mRNA sequence.
ACCESSION CD523457
VERSION   CD523457.1 GI:31455175
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: sgabbs-x@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM205 row: c column: 07
High quality sequence stop: 518.
FEATURES             source
Location/Qualifiers
1..531
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/db_xref="taxon:9606"
/clone="IMAGE:30412182"
/tissue_type="Pooled"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_191"
/notes="vector: pNR-LIB; site_1: Sfil (ggccattatggcc);
Site 2: Sfil (ggcgctcgcc); Library is oligo-dT primed
and directionally cloned. PBMC - Peripheral Blood
Mononuclear Cells. RNA was pooled from 3/6hour stimulation
with PMA adn Ionomycin. 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CACGCCCATATGACC-3' and 3' adaptor sequence:
5'-ATTCTAGCGCGGGCGGCAGATG-dt(30)/BN-3' (where B = A,
C, G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

Qy      1 ATGCGCGCAGGATGGATGGATACCCCGCGGCACCAACAGCGCGCGGCAAGAG 60
Db      23 ATGCGCGCAGGATGGATGGATACCCCGCGGCACCAACAGCGCGCGGCAAGAG 82

us-09-541-462b-1.rst

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Qy      61 CCGTTTGAAGTGAAAAAGTGGAAATCAGTAGCCCTCTGGGCTTGGGATATTGTGTTGAT 120
Db      83 CCGTTTGAAGTGAAAAAGTGGAAATCAGTAGCCCTCTGGGCTTGGGATATTGTGTTGAT 142
Qy      121 AACTGTGCCATCTGCAGNACCACATTATGGATCTTTCATAGATGTCAAGCTAACCCAG 180
Db      143 AACTGTGCCATCTGCAGNACCACATTATGGATCTTTCATAGATGTCAAGCTAACCCAG 202
Qy      181 GCGTCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 240
Db      203 GCGTCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 262
Qy      241 TTCCACTGATCTCTCGCTGGTCAAAACACGACAGGTGTGTCCTATGGACACAGAGAG 300
Db      263 TTCCACTGATCTCTCGCTGGTCAAAACACGACAGGTGTGTCCTATGGACACAGAGAG 322
Qy      301 TGGGAATTCAAAAGTATGGCACTAG 327
Db      323 TGGGAATTCAAAAGTATGGCACTAG 349

RESULT 14
BU729963
LOCUS   BU729963/c
DEFINITION UI-E-CK1-afi-h-19-0-UI.s1 UI-E-CK1 Homo sapiens cDNA clone
IMAGE:30412182 5', mRNA sequence.
ACCESSION BU729963
VERSION   BU729963.1 GI:23653376
KEYWORDS EST.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: sgabbs-x@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM205 row: c column: 07
High quality sequence stop: 518.
FEATURES             source
Location/Qualifiers
1..531
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/db_xref="taxon:9606"
/clone="IMAGE:30412182"
/tissue_type="Pooled"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_191"
/notes="vector: pNR-LIB; site_1: Sfil (ggccattatggcc);
Site 2: Sfil (ggcgctcgcc); Library is oligo-dT primed
and directionally cloned. PBMC - Peripheral Blood
Mononuclear Cells. RNA was pooled from 3/6hour stimulation
with PMA adn Ionomycin. 5' and 3' adaptors were used in
cloning as follows: 5' adaptor sequence:
5'-CACGCCCATATGACC-3' and 3' adaptor sequence:
5'-ATTCTAGCGCGGGCGGCAGATG-dt(30)/BN-3' (where B = A,
C, G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

Qy      1 ATGCGCGCAGGATGGATGGATACCCCGCGGCACCAACAGCGCGCGGCAAGAG 60
Db      23 ATGCGCGCAGGATGGATGGATACCCCGCGGCACCAACAGCGCGCGGCAAGAG 82

us-09-541-462b-1.rst

```

to an EcoR I adaptor, digested with Not I, and cloned directionally into pMT3-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).
TAG_TISSUE=Foveal and Macular Retina
TAG_LIB=UI-E-CK1
TAG_SEQ=GTCC"

ORIGIN

Query Match 100.0%; Score 327; DB 5; Length 533;
Best Local Similarity 100.0%; Pred. No. 3.5e-91;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCGGAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
Db 518 ATGGCGGAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 459
QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db 458 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 399
QY 121 AACTGTGCGATCTGCAGAACACATATATGATCTTTTGCATAGATGTCAAGCTAACCG 180
Db 398 AACTGTGCGATCTGCAGAACACATATATGATCTTTTGCATAGATGTCAAGCTAACCG 339
QY 181 GGTCCCGTACTTTCAGAGAGTGTACTGCGCATGGGAGTGTGCAATTCGACAAACAGAG 240
Db 338 GGTCCCGTACTTTCAGAGAGTGTACTGCGCATGGGAGTGTGCAATTCGACAAACAGAG 279
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGAGTGTGTCCATTGGACAAACAGAG 300
Db 278 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGAGTGTGTCCATTGGACAAACAGAG 219
QY 301 TGGGAATTCCTCAAAAGTATGGGCACTAG 327
Db 218 TGGGAATTCCTCAAAAGTATGGGCACTAG 192

RESULT 15

BG478622 537 bp mRNA linear EST 21-MAR-2001
LOCUS 602525509F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4643619 5',
DEFINITION mRNA sequence.

ACCESSION BG478622.1 GI:13410901

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 537)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILLNL at:

http://image.llnl.gov

Plate: LLCW1414 row: b column: 04

High quality sequence stop: 534.

Location/Qualifiers

1..537

/organism="Homo sapiens"

/mol_type="mRNA"

FEATURES

source

/db_xref=taxon:9606"
/clones=IMAGE:4643619"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_20"
/note=Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 327; DB 4; Length 537;
Best Local Similarity 100.0%; Pred. No. 3.5e-91;
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCGGAGCGATGGATGGATACCCGAGCGGCACCAACAGCGCGCGGCAAGAAG 60
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QY 61 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 120
Db 79 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 138
QY 121 AACTGTGCGATCTGCAGAACACATATATGATCTTTTGCATAGATGTCAAGCTAACCG 180
Db 139 AACTGTGCGATCTGCAGAACACATATATGATCTTTTGCATAGATGTCAAGCTAACCG 198
QY 181 GGTCCCGTACTTTCAGAGAGTGTACTGCGCATGGGAGTGTGCAATTCGACAAACAGAG 240
Db 199 GGTCCCGTACTTTCAGAGAGTGTACTGCGCATGGGAGTGTGCAATTCGACAAACAGAG 258
QY 241 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGAGTGTGTCCATTGGACAAACAGAG 300
Db 259 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGAGTGTGTCCATTGGACAAACAGAG 318
QY 301 TGGGAATTCCTCAAAAGTATGGGCACTAG 327
Db 319 TGGGAATTCCTCAAAAGTATGGGCACTAG 345

Search completed: June 24, 2005, 06:33:53

Job time : 2188 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 24, 2005, 06:37:52 ; Search time 3372 Seconds
(without alignments)
1551.946 Million cell updates/sec

Title: US-09-541-462B-2

Perfect score: 616
Sequence: 1 MAAMDVDPSTGNSGAGKK.....KTRQVCPLDNRWEFQKYG 108

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV=xlh
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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	616	100.0	327	9 AF142059	Homo sapi
2	616	100.0	433	6 CQ698451	Sequence
3	616	100.0	453	6 CQ690099	Sequence
4	616	100.0	467	6 CQ695007	Sequence

5	616	100.0	471	6	CQ712328	Sequence
6	616	100.0	472	6	CQ711142	Sequence
7	616	100.0	482	6	AX888031	Sequence
8	616	100.0	482	6	BD027641	Sequence
9	616	100.0	504	6	BD271522	VonHippel
10	616	100.0	504	10	AF140599	Mus muscu
11	616	100.0	507	6	CQ729899	Sequence
12	616	100.0	508	6	BD271520	VonHippel
13	616	100.0	508	9	AF140598	Homo sapi
14	616	100.0	514	5	BC082183	Xenopus l
15	616	100.0	523	6	CQ701366	Sequence
16	616	100.0	531	10	BC051473	Mus muscu
17	616	100.0	535	9	BC001466	Homo sapi
18	616	100.0	535	9	CR456560	Homo sapi
19	616	100.0	554	9	BC017370	Homo sapi
20	616	100.0	1612	10	BC056992	Mus muscu
21	616	100.0	1616	10	BC027396	Mus muscu
22	610	99.0	153274	2	AY555280	Mus muscu
23	605	98.2	536	5	BC081497	Danio rer
24	605	98.2	172747	2	AC112970	Mus muscu
25	604	98.1	1933	5	AY027936	Salmo sal
26	603	97.9	430	6	CQ709825	Sequence
27	603	97.9	484	5	CR390140	Gallus ga
28	603	97.9	503	6	CQ832496	Sequence
29	586	95.1	4476	6	CQ493737	Sequence
30	584	94.8	497	9	HMYQ60A05	Homo sapi
31	573	93.0	5347	6	AX281690	Sequence
32	554	89.9	3484	9	HSTEST	X73608 H. sapiens m
33	545	88.5	306	9	AY099360	Homo sapi
34	545	88.5	468	6	CQ702730	Sequence
35	535	86.9	692	6	CQ603273	Sequence
36	535	86.9	1181	3	AY119265	Sequence
37	526.5	85.5	830	3	AK116119	Ciona int
38	526	85.4	582	8	BT009441	Triticum
39	524.5	85.1	703	8	AK119792	Oryza sat
40	524.5	85.1	721	8	AK059300	Oryza sat
41	524.5	85.1	1715	8	AK099287	Oryza sat
42	523	84.9	687	8	AY302066	Populus t
43	520.5	84.5	690	8	AK073331	Oryza sat
44	515.5	83.7	635	8	AY086913	Arabidops
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ALIGNMENTS

RESULT 1
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LOCUS AF142059 Homo sapiens RING finger protein (ROCI) mRNA, complete cds.
DEFINITION AF142059 327 bp mRNA linear PRI 14-JUL-1999
ACCESSION AF142059
VERSION AF142059.1 GI:4809215
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 327)
AUTHORS Ohta, T., Michel, J.J., Schottelius, A.J. and Xiong, Y.
TITLE ROCI, a homolog of APC11, represents a family of cullin partners with an associated ubiquitin ligase activity
JOURNAL Mol. Cell 3 (4), 535-541 (1999)
MEDLINE 99247022
PUBMED 10230407
REFERENCE 2 (bases 1 to 327)
AUTHORS Ohta, T., Michel, J.J. and Xiong, Y.
TITLE Direct Submission
JOURNAL Submitted (10-APR-1999) Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill, Mason Farm Rd. and Manning Dr., Chapel Hill, NC 27599-7295, USA

FEATURES
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/organism="Homo sapiens"
/mol_type="mRNA"

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Db 144 AACTGTGCCATCTGCAGGAACACATATGATCTTTGTCATAGATGTCAAGCTAACACAG 203
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QY 61 AlaSerAlaThrSerGluCysThrValAlaTTPGlyValCysAsnHisAlaPheHis 80
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Db 204 GGTCCGCTACTTCAGAAAGTGTACTGCGCATGGGAGTCTGTAAACCATCTTTTCAC 263
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QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
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Db 264 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGAGTGTGTCCATTGGACACACAGAGAG 323
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RESULT 4
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LOCUS CQ695007 467 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 39933 from Patent WO02070737.
ACCESSION CQ695007
VERSION CQ695007.1 GI:42240530
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 39933 12-SEP-2002;
ChondroGene Inc. (CA)
FEATURES
source
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/organism="Homo sapiens"
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Alignment Scores:
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Score: 616.00 Matches: 108
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QY 61 AlaSerAlaThrSerGluCysThrValAlaTTPGlyValCysAsnHisAlaPheHis 80
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QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
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QY 101 TrpGluPheGlnLysTyrGlyHis 108
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Db 320 TGGGAATTCAAAAGTATGGGCAC 343

RESULT 5
CQ712328
LOCUS CQ712328 471 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 57254 from Patent WO02070737.
ACCESSION CQ712328
VERSION CQ712328.1 GI:42273185
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 57254 12-SEP-2002;
ChondroGene Inc. (CA)
FEATURES
source
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ORIGIN
Alignment Scores:
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Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
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DB: 6 Gaps: 0
US-09-541-462B-2 (1-108) x CQ712328 (1-471)

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QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTTPAlaTTPAspIleValValAsp 40
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Db 77 CGCTTTGAAGTGAAGAGTGAATGAGTACAGTAGCCCTCTGGCCCTGGGATATTGTGGTTGAT 136
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QY 41 AnCysAlaIleCysArgHsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
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Db 137 AACTGTGCCATCTGCAGGAACACATATGATCTTTGTCATAGATGTCAAGCTAACACAG 196
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QY 61 AlaSerAlaThrSerGluCysThrValAlaTTPGlyValCysAsnHisAlaPheHis 80
|||||
Db 197 GCGTCCGCTACTTCAGAAAGTGTACTGCGCATGGGAGTCTGTAAACCATCTTTTCAC 256
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QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
|||||
Db 257 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGAGTGTGTCCATTGGACACACAGAGAG 316
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QY 101 TrpGluPheGlnLysTyrGlyHis 108
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Db 317 TGGGAATTCAAAAGTATGGGCAC 340
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RESULT 6
CQ711142
LOCUS CQ711142 472 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 56068 from Patent WO02070737.
ACCESSION CQ711142
VERSION CQ711142.1 GI:42271999
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
TITLE Compositions and methods relating to osteoarthritis


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Pred. No.: 1,41e-58 Length: 482
Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-541-462B-2 (1-108) x BD027641 (1-482)

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DB 89 CGCTTTGAAGTGAAAGAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT 148
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuGluCysGlnAlaAsnGln 60
DB 149 AACTGTGCCATCTGCAGAACACACATTATGGATCTTTGTATAGATGTCAAGCTAACCCAG 208
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 209 GCGTCGCTACTTCAGAGAGTGACTGTCGATCGGAGTCTGTAAACCATGCTTTTTCAC 268
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 269 TTCCACTGCATCTCGCTGGGTCAAAACACGACAGGTGTGTCCATTGGACAAACAGAGAG 328
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DB 329 TGGGAATTCAAAAGTATGGGCAC 352

RESULT 9
BD271522 504 bp DNA linear PAT 17-JUL-2003
LOCUS VonHippel-Lindau tumor suppressor complex and novel component of
DEFINITION SCF ubiquitin ligase.
ACCESSION BD271522
VERSION BD271522.1 GI:33081290
KEYWORDS JP 2002541775-A/3.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLES Conaway, J.W., Conaway, R.C. and Kamura, T.
JOURNAL VonHippel-Lindau tumor suppressor complex and novel component of
COMMENT SCF ubiquitin ligase
PATENT: JP 2002541775-A 3 10-DEC-2002;
OKLAHOMA MEDICAL RESEARCH FOUNDATION
OS Mus sp. (murine)
PN JP 2002541775-A/3
PD 10-DEC-2002
PF 23-FEB-2000 JP 2000601023
PR 26-FEB-1999 US 60/121787
PI JOAN W CONAWAY, RONALD C CONAWAY, TAKUMI KAMURA PC
C12N15/09, A61K38/00, A61K38/53, A61K45/00, A61P35/00, C07K14/47, PC
C12N1/15,
PC
C12N1/19, C12N1/21, C12N5/10, C12N9/00, C12P21/02, G01N33/15, G01N33/ PC
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PC G01N33/68
CC VonHippel-Lindau tumor suppressor complex and novel component
CC of SCF
CC ubiquitin ligase
FH Key Location/Qualifiers
FT source 1..504
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/db_xref="taxon:10095"

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Pred. No.: 1,47e-58 Length: 504
Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-541-462B-2 (1-108) x BD271522 (1-504)

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QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
DB 78 CGCTTTGAAGTTAAAGTGAATGCAGTGGCCCTCTGGGCCCTGGGATATTGTGGTTGAT 137
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuGluCysGlnAlaAsnGln 60
DB 138 AACTGTGCCATCTGCAGAACACACATTATGGATCTTTGTATCGATGTTCAGGCCAACCCAG 197
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DB 198 GCGTCAGCTACTTCGAGAGAGTGTACGGTTGCATGGGAGTCTGCAACCATGCTTTTTCAT 257
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 258 TTCCACTGCATCTCTCGATGGTCAAAACAGAGCGGAGGTGTGTCCGTTGGACAAACAGAGAG 317
QY 101 TrpGluPheGlnLysTyGlyHis 108
DB 318 TGGGAGTTCAGAGTATGGGCAT 341

RESULT 10
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LOCUS Mus musculus ring-box protein 1 (Rbx1) mRNA, complete cds.
DEFINITION
ACCESSION AF140599
VERSION AF140599.1 GI:4769005
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLES Kamura, T., Koepf, D.M., Conrad, M.N., Skowrya, D., Moreland, R.J.,
Iliopoulos, O., Lane, W.S., Kaelin, W.G. Jr., Ellledge, S.J.,
Conaway, R.C., Harper, J.W. and Conaway, J.W.
JOURNAL Rbx1, a component of the VHL tumor suppressor complex and SCF
COMMENT ubiquitin ligase
PATENT: Science 284 (5414), 657-661 (1999)
OS Mus musculus
PN 10213691
PD 99234320
PF 10213691
PR 2 (bases 1 to 504)
PI Kamura, T., Lane, W.S., Conaway, R.C. and Conaway, J.W.
PC Direct Submission
JOURNAL Submitted (05-APR-1999) Prog. Molec. Cell Biol., HHMI, Oklahoma
Med. Res. Fdn., 825 NE 13th St, Oklahoma City, OK 73104, USA
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ORIGIN
Alignment Scores:
Pred. No.: 1.47e-58 Length: 504
Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

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DB 78 CGCTTTGAAGTTAAAGTGAATGCAGTGGCCCTCTGGGCGCTGGGACATTGTGGTTGAT 137
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
DB 138 AACTGTGCCATCTGCAGGACCAACATATTATGGATCTTTGTATCGAATGTTCAGGCCAACAG 197
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QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 258 TTCCACTGCATCTCGATGGCTCAAAACGAGGAGGTGTGTCGTTGGACACACAGAGAG 317
QY 101 TrpGluPheGlnLysTrpGlyHis 108
DB 318 TGGGAGTTCCAGAAGTATGGGCAT 341

RESULT 11
LOCUS CQ729899 507 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 15833 from Patent WO02068579.
ACCESSION CQ729899
VERSION CQ729899.1 GI:42302243
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits for nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 15833 06-SEP-2002;
PE Corporation (NY) (US)
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Best Local Similarity: 100.00% Mismatches: 0

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DB 127 AACTGTGCCATCTGCAGGACCAACATATTATGGATCTTTGCATAGATGTCAACCTAACACAG 186
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 187 GCGTCCGCTACTTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 246
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DB 247 TTCCACTGCATCTCTCGCTGGCTCAAAACGAGGAGTGTGTCATTTGGACACACAGAGAG 306
QY 101 TrpGluPheGlnLysTrpGlyHis 108
DB 307 TGGGAGTTCCAAAAGTATGGGCAC 330

RESULT 12
LOCUS BD271520 508 bp DNA linear PAT 17-JUL-2003
DEFINITION VonHippel-Lindau tumor suppressor complex and novel component of
SCF ubiquitin ligase.
ACCESSION BD271520
VERSION BD271520.1 GI:33081288
KEYWORDS JP 2002541775-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 508)
AUTHORS Conaway,J.W., Conaway,R.C. and Kamura,T.
TITLE VonHippel-Lindau tumor suppressor complex and novel component of
SCF ubiquitin ligase
JOURNAL Patent: JP 2002541775-A 1 10-DEC-2002;
OKLAHOMA MEDICAL RESEARCH FOUNDATION
COMMENT OS Homo sapiens (human)
PN JP 2002541775-A/1
PD 10-DEC-2002
PF 25-FEB-2000 JP 2000601023
PR 26-FEB-1999 US 60/121787
PI JOAN W CONAWAY, RONALD C CONAWAY, TAKUMI KAMURA PC
C12N15/09,A61K38/00,A61K38/53,A61K45/00,A61P35/00,C07K14/47, PC
C12N1/15,
PC
C12N1/19,C12N1/21,C12N5/10,C12N9/00,C12P21/02,G01N33/15,G01N33/ PC
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PC VonHippel-Lindau tumor suppressor complex and novel component
of SCF
CC ubiquitin ligase
CC Key Location/Qualifiers
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Alignment Scores:

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Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
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 Butterfield,Y.S., Krzyzinski,M.I., Skalska,U., Smalilus,D.E.,
 Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 1247932
 3 (bases 1 to 514)
 Klein,S. and Gerhard,D.S.
 Direct Submission
 Submitted (01-SEP-2004) National Institutes of Health, Xenopus Gene
 Collection (XGC), National Institute of Child Health and Human
 Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
 20892-7510, USA
 NIH-MGC Project
 Contact: XGC help desk
 Email: cgabs-x@mail.nih.gov
 Tissue Procurement: Dr. Igor Dawid
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: http://www-shgc.stanford.edu
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
 Series: IRAC Plate: 189 Row: f Column: 1
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Similarity but not
 identity to protein.

FEATURES
 source

Location/Qualifiers
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CDS

ORIGIN

Alignment Scores:
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 Best Local Similarity: 100.00% Mismatches: 0
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 LOCUS
 DEFINITION Sequence 46292 from Patent WO02070737.
 ACCESSION CQ701366
 VERSION CQ701366.1 GI:42262133
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 Liew,C.C., Marshall,W.E. and Zhang,H.
 AUTHORS
 TITLE Compositions and methods relating to osteoarthritis
 JOURNAL Patent: WO 02070737-A 46292 12-SEP-2002;
 Chondrogene Inc. (CA)
 FEATURES
 Location/Qualifiers
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 Score: 616.00 Matches: 108
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 Best Local Similarity: 100.00% Mismatches: 0
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

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Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	616	100.0	506	12	Adq87496 Human tum
5	616	100.0	506	12	Adq87156 Human tum

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c 11	607	98.5	4543	11	ACN90161
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13	603	97.9	539	5	AAH97860
14	603	97.9	586	5	AAH97862
15	596	96.8	380	8	ABX39512
c 16	586	95.1	4476	5	ABV25615
17	576	93.5	485	3	AAA43288
c 18	573	93.0	5347	6	AA94844
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c 20	554	89.9	3484	12	ADQ18564
c 21	554	89.9	3484	13	ADQ80865
c 22	554	89.9	5111	10	ADB75558
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25	535	86.9	692	4	ABL22527
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28	523.5	85.0	531	10	ADK56888
29	523.5	85.0	586	10	ADK56887
30	523.5	85.0	617	10	ADK56882
31	523.5	85.0	691	10	ADK56880
32	521	84.6	683	10	ADK56878
33	520	84.4	673	10	ADK56879
c 34	519.5	84.3	553	13	ACN55764
35	519.5	84.3	608	13	ADR59906
36	515.5	83.7	390	6	ABQ85150
37	515.5	83.7	635	3	AAQ39854
38	514.5	83.5	544	13	ADR59907
39	513.5	83.4	731	10	ADK56881
40	507.5	82.4	831	13	ADR61971
c 41	507	82.3	1050	10	ADD17060
c 42	507	82.3	1050	10	ADD17933
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ALIGNMENTS

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ID AAA96882 standard; DNA; 327 BP.

AC AAA96882;

XX
DT 19-FEB-2001 (first entry)

XX Nucleotide sequence of human ring finger protein ROC1.

DE ROC1; ROC2; cullin; ring finger protein; APC11; APC complex; SCF pathway;
KW cullin dependent ubiquitin ligase; CDK inhibitor Sic1 degradation;
KW tumour; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

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XX WO200058472-A2.

PD 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US008592.

PR 31-MAR-1999; 99US-0127261P.

PR 22-NOV-1999; 99US-0166927P.


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DNA     AAA74980 standard; DNA; 504 BP.
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AC      AAA74980;
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DT      02-JAN-2001 (first entry)
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DE      DNA encoding a murine cullin-interacting RING-H2 finger protein (Rbx1).
XX
KW      Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;
KW      tumour suppressor; carcinoma; Ring box associated carcinoma;
KW      von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;
KW      cerebellar hemangioblastoma; hemangioma; retinal angiomas;
KW      pheochromocytomas; ss.
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OS      Mus sp.
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XX      WO200050445-A1.
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PD      31-AUG-2000.
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PF      25-FEB-2000; 2000WO-US004838.
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PR      26-FEB-1999; 99US-0121787P.
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XX      (OKLA-) OKLAHOMA MEDICAL RES FOUND.
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XX      Conaway JA, Conaway RC, Kamura T;
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DR      WPI; 2000-572067/53.
XX
PT      Cullin interacting RING-H2 finger protein, a component of von Hippel-
PT      Lindau tumor suppressor complex and Skp1-Cdc53p-F-box protein (SCF)
PT      ubiquitin ligase, useful for diagnosing and treating Ring box protein
PT      associated carcinomas.
XX
PS      Disclosure; Page 35; 37pp; English.
XX
CC      The present sequence encodes a murine cullin-interacting RING-H2 finger
CC      protein (Ring box protein), designated Rbx1. The human Rbx1 polypeptide
CC      is a tumour suppressor. Human Rbx1 is useful for diagnosing a
CC      predisposition of a patient to certain carcinomas. It is also useful for
CC      treating Ring box protein associated carcinomas or augmenting
CC      metabolically deficient system in animals. Human Rbx1 is also useful for
CC      evaluating the effectiveness of a therapeutic treatment for Ring box
CC      associated carcinomas. Human Rbx1 can be used to screen for agents which
CC      augment or inhibit the activity of other cullin-containing ubiquitin
CC      ligase and of the VHL (von Hippel-Lindau) complex controlling the
CC      conjugation of ubiquitin or ubiquitin-like proteins to various sets of
CC      target proteins. Carcinomas which may be treated include renal
CC      carcinomas, cerebellar hemangioblastomas and hemangiomas, retinal
CC      angiomas and pheochromocytomas
XX
SQ      Sequence 504 BP; 117 A; 107 C; 137 G; 143 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      3,86e-66      Length:      504
Score:          616.00      Matches:      108
Percent Similarity: 100.00%      Conservative: 0
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Query Match:    100.00%      Indels:      0
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Qy      21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
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Db      138 AACTGTGCCATCTCGAGGAACCAACATTATGATCTTTGTATCGAATGTTCAGGCCAACAG 197
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Db      318 TGGGAGTTCACAGAAGTATGGGCAT 341
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RESULT 4
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ID      ADQ87496 standard; cDNA; 506 BP.
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AC      ADQ87496;
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DT      07-OCT-2004 (first entry)
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DE      Human tumour-associated antigenic target (TAT) cDNA sequence #4374.
XX
KW      human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW      cancer; cell proliferative disorder; gene; ss.
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OS      Homo sapiens.
XX
XX      WO2004060270-A2.
PN
XX
PD      22-JUN-2004.
XX
PF      15-OCT-2003; 2003WO-US029126.
XX
PR      18-OCT-2002; 2002US-0418988P.
XX
XX      (GETH ) GENENTECH INC.
PA
PA      (WUTD/) WU T D.
PA      (ZHOU/) ZHOU Y.
XX
PI      Wu TD, Zhou Y;
XX
XX      WPI; 2004-534300/51.
DR
XX
PT      New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT      preventing or treating cell proliferative disorders such as cancer.
XX
PS      Claim 1; SEQ ID NO 4374; 5504pp; English.
XX
CC      The present invention describes an isolated tumour-associated antigenic
CC      target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
CC      sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of
CC      (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC      sequence identity to (a)-(c); or (e) a sequence that hybridises to (a) -
CC      (c). Also described: (1) an expression vector comprising the above
CC      nucleic acid; (2) a host cell comprising the above expression vector; (3)
CC      a process for producing a polypeptide; (4) an isolated polypeptide
CC      comprising: (a) an amino acid sequence encoded by any of the above
CC      nucleotide sequences; (b) an amino acid sequence encoded by the full-
CC      length coding region of the above nucleotide sequences; or (c) a sequence
CC      having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
CC      comprising the above polypeptide fused to a heterologous polypeptide; (6)
CC      an isolated antibody that binds to the above polypeptide; (7) a process
CC      for producing the antibody; (8) an isolated oligopeptide that binds to
CC      the above polypeptide; (9) a tumour-associated antigenic target (TAT)
CC      binding organic molecule that binds to the above polypeptide; (10) a
CC      composition of matter comprising the above (chimeric) polypeptide,

```

antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;

Alignment Scores:		
Pred. No.:	3,898-66	Length:
Score:	616.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	100.00%	Indels:
DB:	12	Gaps:

US-09-541-462B-2 (1-108) x ADQ87496 (1-506)

Qy	1	MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys	20
Db	6	ATGGCGGCAGCATGTGATGTGATACCCGAGCGGCACCAACAGCGCGCGGCACGAAGAAG	65
Qy	21	ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp	40
Db	66	CGCTTTGAAGTCAAAAAGTGAATGCACGTACCTCTGGGCTGGGATATTGTGGTTGAT	125
Qy	41	AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnIleAsnGln	60
Db	126	AACTGTGCCATCTGCAGGAACACACATTATGATCTTTGCATAGAAATGTCAAGCTAACCCAG	185
Qy	61	AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis	80
Db	186	GGGTCCGCTACTTCAGAGAGGTGTACTCTGCATGGGGAGTCTGTAACCATGCTTTTCAC	245
Qy	81	PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu	100
Db	246	TTCCACTGCATCTCTCGCTGGGCTCAAAACACGACAGAGGTGTCTCATTTGGACAACAGAGAG	305
Qy	101	TrpGluPheGlnLysTrpGlyHis	108
Db	306	TGGGAATTCAAAAGTATGGGCAC	329

RESULT 5

ADQ87156
ID ADQ87156 standard: cDNA; 506 BP.

XX
AC ADO87156:

XX
DT 07-OCT-2004 (first entry)

XX Human tumour-associated antigenic target (TAT) cDNA sequence #4032.

xx human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
kw cancer; cell proliferative disorder; gene; ss.

XX Homo sapiens.
OS

XX

XX	22-JUL-2004.
PD	
XX	15-OCT-2003; 2003WO-US029126.
PF	
XX	18-OCT-2002; 2002US-0418988P.
PR	
XX	(GETH) GENENTECH INC.
PA	(WUTD/) WU T D.
PA	(ZHOU/) ZHOU Y.
XX	
PI	Wu TD, Zhou Y;
XX	
DR	WPI; 2004-534300/51.
XX	
XX	New nucleic acid molecule and encoded polypeptide, for diagnosing and preventing or treating cell proliferative disorders such as cancer.
PT	
PT	Claim 1; SEQ ID NO 4032; 5504bp; English.
PS	

The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

XX
S0 Semence 506 BP: 126 A: 105 C: 124 G: 151 T: 0 U: 0 Other:

Alignment Scores:		
Pred. No.:	3,898-66	506
Score:	616.00	108
Percent Similarity:	100.00%	0
Best Local Similarity:	100.00%	0
Query Match:	100.00%	0
DB:	12	0
	Length:	
	Matches:	
	Conservative:	
	Mismatches:	
	Indels:	
	Gaps:	

US-09-541-462B-2 (1-108) X ADO87156 (1-506)

1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20

6	ATGCGGCGACGATGGATGTGGATACCCGAGCGGCACCAACACGCGCGCGGCGAAGAAG	65
21	ArgPheGluValLysLeuTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp	40
66	CGCTTTGAAGTGAANAAGTGGAAATGCAGTAGCCCTCTGGGCCTGGGATATTGTGGTTGAT	125
41	AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln	60
126	AACTGTGCCATCTGCAGGACCACATATGATGATCTTTCATAGAAATGTCAAAGCTAACCCAG	185
61	AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis	80
186	GGTCCGCTACTTTCAGAAAGTGTACTGTGCATGGGGAGTCTGTAAACCATGCTTTTCAC	245
81	PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu	100
246	TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGGTGTGTCCATTGGCAACACAGAGAG	305
101	TrpGluPheGlnLysTyrGlyHis	108
306	TGGGAATTCCAAAGATATGGGCAC	329

RESIST 6

RESULTS 6
ADQ84881
ID ADQ84881 standard: cDNA: 506 BP.

AC ADQ84881;

DT 07-OCT-2004 (first entry)

DE Human tumour-associated antigenic target (TAT) cDNA sequence #1695.

human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW
cancer; cell proliferative disorder; gene; ss.
KW

OS Homo sapiens.

WO2004060270-A2.

22-JUL-2004.

15-OCT-2003; 2003WO-US029126.

PR 18-OCT-2002; 2002US-0418988P.

PA (GETH) GENENTECH INC.

PA (ZHOU//) ZHOU Y.
PA (ZHOU//) ZHOU Y.

PI Wu TD, Zhou Y:

WPI: 2004-534300

XX New nucleic acid mol

PS Claim 1: SEQ ID NO 1695: 5504bp: English.
XX preventing or treating cell proliferative disorders such as cancer

CC The present invention describes an isolat

target (ant), nucleotide comprising: (a) any of 4822 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a) - (c); or (e) a sequence that hybridizes to (a) - (c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identical to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) an isolated oligopeptide that binds to the above antibody.

the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

SQ Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;

Alignment Scores:	
Pred. No.:	3,898-66
Pred. No.:	616.00
Length:	506
Matches:	108
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0
DB:	13
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%

US-09-541-462B-2 (1-108) x ADO84881 (1-506)

Qy		20	1	MetAlaIalalaMetAspValAepThrProSerGlyThrAsnSerGlyAlaGlyLysLys	20
Dd		65	6	ATGCGGCAGCGATGGATGTGGATATCCCGACGCGCAACAACAGCGCGCGCGCAAGAAG	65
Qy		40	21	ArgPheGluValLysLysTTPAsnAlavalalaleuTrpAlatrpAspIleValValAasp	40
Dd		125	66	CGCTTTGAAGTGAAAAAGTGGAAATGSCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGAT	125
Qy		60	41	AsnCysAlalleCysArGAsnHisIleMetAspLeuCysIleGluCysclnAlaAsnGln	60
Dd		185	126	AACGTGCCATCTCGAGAACCAATTATGGATCTTCATAGATAATGCAAGCTTAACCAG	185
Qy		80	61	AlaSerAlathrSerGluGluCysThrValAlatrpglyValCysAsnHisAlaPheHis	80
Dd		245	186	GCGTCCGCTACTTCAGAAAGATGTACTGTCCATGGGGAGTCTGTAAACATGCTTTTCA	245
Qy		100	81	PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu	100
Dd		305	246	TTCCACTGCATCTCTCGCTGGCTCAAACACGACAGGTGTGTGCCATTGACCAACAGAGAG	305
Qy			101	TrpGluPheGlnLysTyrGlyHis	108
Dd			306	TGGGAATTCAAAAGATATGGGCAC	329

RESULT 7

AAA74978

ID AAA74978 standard; DNA; 508 BP.

AC AAA74978;

DT 02-JAN-2001 (first entry)

DE DNA encoding a human cullin

KW Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;
 KW tumour suppressor; carcinoma; Ring box associated carcinoma;
 KW von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;

KW cerebellar hemangioblastoma; hemangioma; retinal angioma;
 XX pheochromocytomas; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..333
 FT /*tag= a
 FT /product= "cullin-interacting RING-H2 finger protein
 FT (Rbx1)"
 XX
 PN WO200050445-A1.
 XX
 PD 31-AUG-2000.
 XX
 PF 25-FEB-2000; 2000WO-US004838.
 XX
 PR 26-FEB-1999; 99US-0121787P.
 XX
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 XX
 PI Conaway JA, Conaway RC, Kamura T;
 XX
 DR WPI; 2000-572067/53.
 DR P-PSDB; AAB08813.
 XX
 PT Cullin interacting RING-H2 finger protein, a component of von Hippel-
 PT Lindau tumor suppressor complex and Skp1-Cdc53p-F-box protein (SCF)
 PT ubiquitin ligase, useful for diagnosing and treating Ring box protein
 PT associated carcinomas.
 XX
 PS Claim 3; Page 35; 37pp; English.
 XX
 CC The present sequence encodes a human cullin-interacting RING-H2 finger
 CC protein (Ring box protein), designated Rbx1. The polypeptide is a tumour
 CC suppressor. Rbx1 is useful for diagnosing a predisposition of a patient
 CC to certain carcinomas. It is also useful for treating Ring box protein
 CC associated carcinomas or augmenting metabolically deficient system in
 CC animals. Rbx1 is also useful for evaluating the effectiveness of a
 CC therapeutic treatment for Ring box associated carcinomas. Rbx1 can be
 CC used to screen for agents which augment or inhibit the activity of other
 CC cullin-containing ubiquitin ligase and of the VHL (von Hippel- Lindau)
 CC complex controlling the conjugation of ubiquitin or ubiquitin- like
 CC proteins to various sets of target proteins. Carcinomas which may be
 CC treated include renal carcinomas, cerebellar hemangioblastomas and
 CC hemangiomas, retinal angioma and pheochromocytomas
 XX
 SQ Sequence 508 BP; 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3,91e-66 Length: 508
 Score: 616.00 Matches: 108
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0
 US-09-541-462B-2 (1-108) x AAA74978 (1-508)
 QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
 DB 7 ATGCGCGCAGCGATGGATGTGGATACCCCGAGCGGCACCAACAGCGCGCGCAAGAG 66
 QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 DB 67 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 126
 QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysGlnAlaAsnGln 60
 DB 127 AACTGTGCGCATCTGCAGGACCAACATTATGATCTTTGCATAGATGTCAGCTAACCG 186
 QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80

Db 187 GCGTCGGCTACTTCAGAAAGAGGTACTGTGCGATGGGGAGTCTGTAAACCATGCTTTTCAC 246
 QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 Db 247 TTCCACTGCATCTCTCGCTGGCTCAAAACACACACAGGTGTGTCATTGGACACAGAGAG 306
 QY 101 TrpGluPheGlnLysTyrglyHis 108
 Db 307 TGGGAATTCCTCAAAAGTATGGGCAC 330
 RESULT 8
 ACN40951
 ID ACN40951 standard; cDNA; 508 BP.
 XX
 AC ACN40951;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Tumour-associated antigenic target (TAT) cDNA DNA326980, SEQ ID NO:6072.
 XX
 KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2004030615-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 29-SEP-2003; 2003WO-US028547.
 XX
 PR 02-OCT-2002; 2002US-0414971P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Wu TD, Zhang Z, Zhou Y;
 XX
 DR WPI; 2004-347921/32.
 DR P-PSDB; ABM82365.
 XX
 PT New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 PS Claim 1; SEQ ID NO 6072; 7273pp; English.
 XX
 CC The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT nucleic acid of the invention
 XX

Sequence 508 BP; 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,91e-66 Length: 508
Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-541-462B-2 (1-108) x ACN40951 (1-508)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyValaGlyLysLys 20
DB 7 ATGGCGCGAGCATGTGATGATACCCCGAGCGGCACCAACAGCGCGCGCAAGAG 66
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspLysValValAsp 40
DB 67 CGCTTTGAAGTGAAAAGTGGAATGCAGTAGCCCTCGGCTGGGATATTGTGGTTGAT 126
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuGluCysGlnAlaAsnGln 60
DB 127 AACTGTGCCATCTGCAGGAACACATATTGGATCTTTGCATAGAAATGTCAAGCTAACCCAG 186
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 187 GCGTCGCTACTTTCAGAAAGTGTAAGTGTGCGATGGGAGTCTGTAAACCATGCTTTTTCAC 246
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 247 TTCACACTGCATCTCTCGTGGCTCAAAACACACAGAGTGTGTCATTTGGACACAGAGAG 306
QY 101 TrpGluPheGlnLysTrpGlyHis 108
DB 307 TGGGAATTCAAAAGTATATGGGCAC 330

RESULT 9

ACH29979
ID ACH29979 standard; cDNA; 476 BP.
XX AC ACH29979;
XX DT 13-OCT-2003 (first entry)
XX DE Human testis cDNA #365.
XX KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
XX KW genome mapping; biodiversity; genetic disorder.
XX OS Homo sapiens.
XX PN US2003073623-A1.
XX PD 17-APR-2003.
XX PF 30-JUL-2001; 2001US-00918995.
XX PR 30-JUL-2001; 2001US-00918995.
XX PA (DRMA/) DRMANAC R T.
XX PA (LABA/) LABAT I.
XX PA (STAC/) STACHE-CRAIN B.
XX PA (DICK/) DICKSON M C.
XX PA (JONE/) JONES L W.
XX PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX DR WPI; 2003-615964/58.
XX PT New polynucleotide sequences obtained from various cDNA libraries, useful
XX PT as hybridization probes, as oligomers for PCR, for chromosome and gene
XX PT mapping, in the recombinant production of protein, or in generating
XX PT antisense DNA or RNA.

XX

PS Claim 1; SEQ ID NO 17191; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030073623

XX Sequence 476 BP; 119 A; 111 C; 124 G; 118 T; 0 U; 4 Other;

Alignment Scores:

Pred. No.: 1.47e-65 Length: 476
Score: 611.00 Matches: 107
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.19% Indels: 0
DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) x ACH29979 (1-476)

QY 2 AlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyValaGlyLysLysArg 21
DB 75 GCGCAGCGATGATGTGGATACCCCGAGCGGCACACAGCGCGCGGCAAGAGCGC 134
QY 22 PheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspLysValValAspAsn 41
DB 135 TTTGAAGTGAAAAGTGGATGCGATGAGTCCCTCTGGGCTGGGATATTGTGTTGATAC 194
QY 42 CysAlaIleCysArgAsnHisIleMetAspLeuGluCysGlnAlaAsnGlnAla 61
DB 195 TGTCCCATCTGCAGGAACCAATATGATCTTTGATAGTAATGTCAAGCTAACCGCG 254
QY 62 SerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPhe 81
DB 255 TCCGCTACTTCAGAAAGATGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCACTTC 314
QY 82 HisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgLysTrp 101
DB 315 CACTGCAATCTCTCGTGGCTCAAAACACAGCAGGTGTGTCCATTGGACACAGAGAGTGG 374
QY 102 GluPheGlnLysTrpGlyHis 108
DB 375 GAATTCAAAAGTATGGGCAC 395

RESULT 10

ADS09913/C
ID ADS09913 standard; DNA; 3726 BP.
XX AC ADS09913;
XX DT 16-DEC-2004 (first entry)
XX DE Human therapeutic DNA - SEQ ID 150.
XX KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
XX KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
XX KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.
XX OS Homo sapiens.
XX

PN WO2004080148-A2.
 XX 23-SEP-2004.
 XX 30-SEP-2003; 2003WO-US030720.
 XX 02-OCT-2002; 2002US-0416186P.
 XX (NUVE-) NUVELO INC.
 XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
 PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
 XX WPI: 2004-668857/65.
 DR P-PSDB; ADS10597.
 XX New polynucleotide, useful in preparing a composition for diagnosing or
 PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
 PT aplastic anemia or cancer for promoting wound healing.
 XX Claim 1; SEQ ID NO 150; 718pp; English.
 XX The invention relates to a novel isolated polynucleotide and the encoded
 CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
 CC neuroprotective, antianaemic, cytostatic and vulnerary activities and may
 CC be useful in preparing a composition for diagnosing or treating
 CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
 CC disorders, such as aplastic anaemia or cancer, as well as for promoting
 CC wound healing. The molecules may also be utilised during gene therapy
 CC procedures. The current sequence is that of a human therapeutic DNA of
 CC the invention. The current sequence is not shown explicitly within the
 CC specification but can be accessed from the WIPO web-site.
 XX Sequence 3726 BP; 996 A; 955 C; 845 G; 930 T; 0 U; 0 Other;
 SQ
 Alignment Scores: Length: 3726
 Pred. No.: 7,64e-64 Matches: 106
 Score: 607.00 Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 98.54% Gaps: 13
 DB: 13
 US-09-541-462B-2 (1-108) x ADS09913 (1-3726)
 QY 3 AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPhe 22
 DB 492 GCAGCGATGGATGGATATCCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 433
 QY 23 GluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCys 42
 DB 432 GAAGTGAAGAAAGTGAATGAGTAGCCCTCTGGGCCTGGGATATGTGGTTGATACTGT 373
 QY 43 AlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSer 62
 DB 372 GCCATCTGCAGGACCAACCATTTATGGATCTTTGGCATAGATGTCAAGCTAACAGGGCTCC 313
 QY 63 AlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHis 82
 DB 312 GCTACTTTCAGAGAGTGTACTGTGCATGGGAGTCTGTAAACCATGCTTTTCACTTCCAC 253
 QY 83 CysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGlu 102
 DB 252 TGCATCTCTGCTGGCTCAAAACACAGACAGTGTGTTCATTTGGACACAGAGAGTGGAA 193
 QY 103 PheGlnLysTyrGlyHis 108
 DB 192 TTCCAAAAGTATGGGCAC 175
 RESULT 11
 ACN90161/c
 ID ACN90161 standard; DNA; 4543 BP.
 XX

AC ACN90161;
 XX 02-DEC-2004 (first entry)
 XX Breast cancer related marker, seq id 11311.
 DE Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
 XX Homo sapiens.
 OS US2003099974-A1.
 PN 29-MAY-2003.
 XX 18-JUL-2002; 2002US-00198846.
 XX 18-JUL-2001; 2001US-0306220P.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Lillie J, Xu Y, Wang Y, Steinmann K;
 PI WPI: 2003-787014/74.
 XX Novel isolated polypeptide associated with breast cancer, useful for
 PT detecting presence of polypeptide in sample, as a marker for breast
 PT cancer.
 XX Disclosure; SEQ ID NO 11311; 36pp; English.
 PS The invention relates to an isolated polypeptide (I) associated with
 CC breast cancer which is encoded by a nucleic acid molecule comprising a
 CC nucleotide sequence (S1). Further disclosed is an antibody that binds to
 CC the polypeptide of the invention. The activity of the polypeptide of the
 CC invention may be described as cytostatic. The antibody is useful for
 CC detecting the presence of (I) in a sample. Nucleic acid molecules of the
 CC invention are useful in the detection of breast tumours. (I) is useful as
 CC a marker for breast cancer and in breast cancer therapy. Sequences given
 CC in records ACN78851-ACN92934 represent nucleic acid markers associated
 CC with breast cancer. Note: The sequence listing does not form part of the
 CC specification but may be obtained in electronic format from the USPTO web
 CC site at seqdata.uspto.gov/sequence.html?docID=20030099974
 XX Sequence 4543 BP; 1069 A; 1171 C; 1083 G; 1220 T; 0 U; 0 Other;
 SQ
 Alignment Scores: Length: 4543
 Pred. No.: 1e-63 Matches: 106
 Score: 607.00 Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 98.54% Gaps: 11
 DB: 11
 US-09-541-462B-2 (1-108) x ACN90161 (1-4543)
 QY 3 AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPhe 22
 DB 1085 GCAGCGATGGATGGATATCCCGAGCGGCACCAACAGCGCGCGGCAAGAGCGCTTT 1026
 QY 23 GluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCys 42
 DB 1025 GAAGTGAAGAAAGTGAATGAGTAGCCCTCTGGGCCTGGGATATGTGGTTGATACTGT 966
 QY 43 AlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSer 62
 DB 965 GCCATCTGCAGGACCAACCATTTATGGATCTTTGGCATAGATGTCAAGCTAACAGGGCTCC 906
 QY 63 AlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHis 82
 DB 905 GCTACTTTCAGAGAGTGTACTGTGCATGGGAGTCTGTAAACCATGCTTTTCACTTCCAC 846
 QY 83 CysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGlu 102

Db 845 TGCATCTCTCGTGGCTCAAAACACGACGAGTGTGTCTTCATTGGACACAGAGAGTGGGAA 786

Qy 103 PheGlnLysTyrGlyHis 108
|||||
Db 785 TTCCAAAAGTAGTGGGCAC 768

RESULT 12

ADQ92179
ID ADQ92179 standard; DNA; 503 BP.

AC ADQ92179;

DT 07-OCT-2004 (first entry)

DE Human autoantigen DNA fragment MPMP800L05536.

KW ds; autoantigen; antibody; hybridoma; biosensor chip;
KW extracorporeal differential diagnosis; autoimmune disease;
KW ribosomal protein; tubulin;
KW dolichyl-diphospho-oligosaccharide-glycosyl transferase;
KW multiple sclerosis; rheumatoid arthritis; epitope mapping;
KW affinity chromatography; electrophoresis; autoantibody adhesion;
KW RNA interference; RNAi.

OS Homo sapiens.

XX WO2004058972-A1.

FN 15-JUL-2004.

XX 23-DEC-2002; 2002WO-EP014731.

PR 23-DEC-2002; 2002WO-EP014731.

PA (THIE/) THIESEN H.

PA (LORE/) LORENZ P.

PI Thiesen H, Lorenz P;

XX WPI; 2004-543459/52.

XX New human DNA autoantigens, useful as assay, diagnostic, and prognostic reagents and for treating autoimmune disease, also related expression products and antibodies with similar uses.

PS Claim 1; SEQ ID NO 160; 110pp; German.

XX This invention describes novel human DNA autoantigens which are used to produce recombinant expression vectors; prokaryotic or eukaryotic cells; poly- or mono-clonal antibodies (Ab) specific; hybridomas that express monoclonal Ab; biosensor chips having an addressable sequence pattern as probes; medical or diagnostic instruments that include the biosensor; for extracorporeal differential diagnosis of autoimmune diseases and predisposition to them. The autoantigen polynucleotides encode ribosomal proteins; tubulins; dolichyl-diphospho-oligosaccharide-glycosyl transferases and proteins. The antibodies may be labelled conventionally with radioisotopes, coloured or fluorescent groups, or a member of the biotin/avidin pair, or colloidal gold. The autoantigens can be directed against mitochondria, liver-kidney microsomes; histidyl-tRNA; nuclear membrane; neutrophilin/cytoplasm; insect cells; epidermal intracellular or basal membrane antigens; Golgi or cell nuclei, or associated with multiple sclerosis or rheumatoid arthritis. They are useful for epitope mapping; in affinity chromatography or electrophoresis; for diagnosis, prognosis, control of treatment or therapeutic response of autoimmune diseases, particularly in vitro differential diagnosis of autoimmune diseases; to produce biosensor chips or for autoantibody adhesion. Autoantigen DNA can be used for therapeutic RNA interference against autoantibodies. Biochips that carry the new materials are useful in medical and diagnostic instruments. ADQ92020-ADQ92280 represent human autoantigens.

XX Sequence 503 BP; 131 A; 102 C; 120 G; 150 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,53e-64 Length: 503
Score: 603.00 Matches: 105
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.89% Indels: 0
DB: 12 Gaps: 0

US-09-541-462B-2 (1-108) x ADQ92179 (1-503)

Qy 4 AlaMetAspValAspThrProSerGlyThrAsnSerGlyValaGlyLysLysArgPheGlu 23
|||||
Db 3 GCGATGGATGTGGATACCCCGCGGCACCAACAGCGCGCGGCAAGAGCGCTTTGAA 62
|||||

Qy 24 VallLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAla 43
Db 63 GTGAAAAAGTGAATGCAGTAGCCCTCTGGGCTCTGGGATATTGTTGATAAATCTGTGCC 122
|||||

Qy 44 IleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAla 63
Db 123 ATCTGCAGGAACCAATATTGGATCTTTGCAATAGAATGTCAAGCTAACCCAGCGCTCCGCT 182
|||||

Qy 64 ThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCys 83
Db 183 ACTTCAGAGAGTGTACTGTGCGATGGGAGTCTGTAAACCATGCTTTTCATCTCCACTGC 242
|||||

Qy 84 IleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPhe 103
Db 243 ATCTCTCGTGGCTCAAAACACGACAGTGTGTCTCATTTGGACAACAGAGAGTGGGAATTC 302
|||||

Qy 104 GlnLysTyrGlyHis 108
Db 303 CAAAAGTATGGGCAC 317
|||||

RESULT 13

AAH97860

ID AAH97860 standard; DNA; 539 BP.

XX AC AAH97860;

XX 10-OCT-2001 (first entry)

DT Murine 7-transmembrane G-protein coupled receptor coding sequence #104.

DE Murine; hematopoietic stem cell; signalling; vaccine; 7TM-GPCR;

KW 7-transmembrane G-protein coupled protein receptor; ds.

XX Mus sp.

XX WO200160999-A1.

XX 23-AUG-2001.

PP 14-FEB-2001; 2001WO-US004700.

XX 14-FEB-2000; 2000US-0182377P.

PA (IMCL-) IMCLONE SYSTEMS INC.

PA (UYPR-) UNIV PRINCETON.

XX Lemischka IR, Witte L, Pereira DS;

PI WPI; 2001-522596/57.

DR DNA Sequences encoding 7-transmembrane G-protein coupled protein receptors characteristic of hematopoietic stem cells, useful for treating leukemia.

XX PT Claim 1; Page 62; 176pp; English.

XX The present invention relates to murine coding sequences for 7-transmembrane G-protein coupled protein receptors (7TM-GPCRs). The present sequence is one such murine 7TM-GPCR coding sequence. The present

CC sequence was derived from hematopoietic stem cells. The present sequence
CC and its corresponding protein are useful in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate 7TM-GPCR expression.
CC 7TM-GPCRs identify specific signalling molecules, to activate an effector
CC -signalling cascade that triggers an intracellular response and
CC eventually a biological effect
XX

SQ Sequence 539 BP; 128 A; 112 C; 150 G; 149 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.68e-64 Length: 539
Score: 603.00 Matches: 105
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.89% Indels: 0
DB: 5 Gaps: 0

US-09-541-462B-2 (1-108) x AAH97860 (1-539)

QY 4 AlaMetAspValAspThrProSerGlyThrAsnSerGlyValAlaGlyLysLysArgPheGlu 23
DB 1 GCATGGATGTGGATACCCCGCGGCACCAACAGCGCGCGGCAAGAGCGCTTTGAA 60
QY 24 ValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAla 43
DB 61 GTTAAAGTGGATGAGTGGGCTCTGGGCTGGGACATTGTGTTGTAACCTGTGC 120
QY 44 IleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAla 63
DB 121 ATCTCGAGGAAACACATTATGGATCTTTGTATCGAATGTGAGGCCAACAGGCGTCAGCT 180
QY 64 ThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisCys 83
DB 181 ACTTCGAAGAGTGTACGGTTGATGGGAGTCTGCAACCATGCTTTTCATTTCCACTGC 240
QY 84 IleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPhe 103
DB 241 ATCTCTCGATGGTCAAAACGAGCGAGGTGTGTCCTGTGGACAAACAGAGTGGGAGTTC 300
QY 104 GlnLysTyrGlyHis 108
DB 301 CAGAAGTATGGGCAT 315

RESULT 14

AAH97862

ID AAH97862 standard; DNA; 586 BP.

XX AC AAH97862;

XX AC

XX AC

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PT DNA Sequences encoding 7-transmembrane G-protein coupled protein
PT receptors characteristic of hematopoietic stem cells, useful for treating
PT leukemia.
XX

PS Claim 1; Page 63; 176pp; English.

XX The present invention relates to murine coding sequences for 7-
CC transmembrane G-protein coupled protein receptors (7TM-GPCRs). The
CC present sequence is one such murine 7TM-GPCR coding sequence. The present
CC sequence was derived from hematopoietic stem cells. The present sequence
CC and its corresponding protein are useful in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate 7TM-GPCR expression.
CC 7TM-GPCRs identify specific signalling molecules, to activate an effector
CC -signalling cascade that triggers an intracellular response and
CC eventually a biological effect
XX

SQ Sequence 586 BP; 140 A; 122 C; 164 G; 159 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 1.89e-64 Length: 586
Score: 603.00 Matches: 105
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.89% Indels: 0
DB: 5 Gaps: 0

US-09-541-462B-2 (1-108) x AAH97862 (1-586)

QY 4 AlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPheGlu 23
DB 1 GCATGGATGTGGATACCCCGCGGCACCAACAGCGCGCGGCAAGAGCGCTTTGAA 60
QY 24 ValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAla 43
DB 61 GTTAAAGTGGATGAGTGGGCTCTGGGCTGGGACATTGTGTTGTAACCTGTGC 120
QY 44 IleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAla 63
DB 121 ATCTCGAGGAAACACATTATGGATCTTTGTATCGAATGTGAGGCCAACAGGCGTCAGCT 180
QY 64 ThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisCys 83
DB 181 ACTTCGAAGAGTGTACGGTTGATGGGAGTCTGCAACCATGCTTTTCATTTCCACTGC 240
QY 84 IleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPhe 103
DB 241 ATCTCTCGATGGTCAAAACGAGCGAGGTGTGTCCTGTGGACAAACAGAGTGGGAGTTC 300
QY 104 GlnLysTyrGlyHis 108
DB 301 CAGAAGTATGGGCAT 315

RESULT 15

ABX39512

ID ABX39512 standard; cDNA; 380 BP.

XX AC ABX39512;

XX AC

XX AC

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XX AC

PT DNA Sequences encoding 7-transmembrane G-protein coupled protein
PT receptors characteristic of hematopoietic stem cells, useful for treating
PT leukemia.
XX

PS Claim 1; Page 63; 176pp; English.

XX The present invention relates to murine coding sequences for 7-
CC transmembrane G-protein coupled protein receptors (7TM-GPCRs). The
CC present sequence is one such murine 7TM-GPCR coding sequence. The present
CC sequence was derived from hematopoietic stem cells. The present sequence
CC and its corresponding protein are useful in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate 7TM-GPCR expression.
CC 7TM-GPCRs identify specific signalling molecules, to activate an effector
CC -signalling cascade that triggers an intracellular response and
CC eventually a biological effect
XX

SQ Sequence 586 BP; 140 A; 122 C; 164 G; 159 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 1.89e-64 Length: 586
Score: 603.00 Matches: 105
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.89% Indels: 0
DB: 5 Gaps: 0

US-09-541-462B-2 (1-108) x AAH97862 (1-586)

QY 4 AlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPheGlu 23
DB 1 GCATGGATGTGGATACCCCGCGGCACCAACAGCGCGCGGCAAGAGCGCTTTGAA 60
QY 24 ValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAla 43
DB 61 GTTAAAGTGGATGAGTGGGCTCTGGGCTGGGACATTGTGTTGTAACCTGTGC 120
QY 44 IleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAla 63
DB 121 ATCTCGAGGAAACACATTATGGATCTTTGTATCGAATGTGAGGCCAACAGGCGTCAGCT 180
QY 64 ThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisCys 83
DB 181 ACTTCGAAGAGTGTACGGTTGATGGGAGTCTGCAACCATGCTTTTCATTTCCACTGC 240
QY 84 IleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPhe 103
DB 241 ATCTCTCGATGGTCAAAACGAGCGAGGTGTGTCCTGTGGACAAACAGAGTGGGAGTTC 300
QY 104 GlnLysTyrGlyHis 108
DB 301 CAGAAGTATGGGCAT 315

RESULT 15

ABX39512

ID ABX39512 standard; cDNA; 380 BP.

XX AC ABX39512;

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

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US2002137139-A1.

XX AC

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XX AC

PT DNA Sequences encoding 7-transmembrane G-protein coupled protein
PT receptors characteristic of hematopoietic stem cells, useful for treating
PT leukemia.
XX

PS Claim 1; Page 63; 176pp; English.

XX The present invention relates to murine coding sequences for 7-
CC transmembrane G-protein coupled protein receptors (7TM-GPCRs). The
CC present sequence is one such murine 7TM-GPCR coding sequence. The present
CC sequence was derived from hematopoietic stem cells. The present sequence
CC and its corresponding protein are useful in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate 7TM-GPCR expression.
CC 7TM-GPCRs identify specific signalling molecules, to activate an effector
CC -signalling cascade that triggers an intracellular response and
CC eventually a biological effect
XX

SQ Sequence 586 BP; 140 A; 122 C; 164 G; 159 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 1.89e-64 Length: 586
Score: 603.00 Matches: 105
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.89% Indels: 0
DB: 5 Gaps: 0

US-09-541-462B-2 (1-108) x AAH97862 (1-586)

QY 4 AlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPheGlu 23
DB 1 GCATGGATGTGGATACCCCGCGGCACCAACAGCGCGCGGCAAGAGCGCTTTGAA 60
QY 24 ValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAla 43
DB 61 GTTAAAGTGGATGAGTGGGCTCTGGGCTGGGACATTGTGTTGTAACCTGTGC 120
QY 44 IleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAla 63
DB 121 ATCTCGAGGAAACACATTATGGATCTTTGTATCGAATGTGAGGCCAACAGGCGTCAGCT 180
QY 64 ThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisCys 83
DB 181 ACTTCGAAGAGTGTACGGTTGATGGGAGTCTGCAACCATGCTTTTCATTTCCACTGC 240
QY 84 IleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPhe 103
DB 241 ATCTCTCGATGGTCAAAACGAGCGAGGTGTGTCCTGTGGACAAACAGAGTGGGAGTTC 300
QY 104 GlnLysTyrGlyHis 108
DB 301 CAGAAGTATGGGCAT 315

RESULT 15

ABX39512

ID ABX39512 standard; cDNA; 380 BP.

XX AC ABX39512;

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

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XX AC

XX AC

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XX AC

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US2002137139-A1.

XX AC

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XX AC

XX AC

XX AC

XX AC

XX AC

PT DNA Sequences encoding 7-transmembrane G-protein coupled protein
PT receptors characteristic of hematopoietic stem cells, useful for treating
PT leukemia.
XX

PS Claim 1; Page 63; 176pp; English.

XX The present invention relates to murine coding sequences for 7-
CC transmembrane G-protein coupled protein receptors (7TM-GPCRs). The
CC present sequence is one such murine 7TM-GPCR coding sequence. The present
CC sequence was derived from hematopoietic stem cells. The present sequence
CC and its corresponding protein are useful in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate 7TM-GPCR expression.
CC 7TM-GPCRs identify specific signalling molecules, to activate an effector
CC -signalling cascade that triggers an intracellular response and
CC eventually a biological effect
XX

SQ Sequence 586 BP; 140 A; 122 C; 164 G; 159 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 1.89e-64 Length: 586
Score: 603.00 Matches: 105
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.89% Indels: 0
DB: 5 Gaps: 0

US-09-541-462B-2 (1-108) x AAH97862 (1-586)

QY 4 AlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPheGlu 23
DB 1 GCATGGATGTGGATACCCCGCGGCACCAACAGCGCGCGGCAAGAGCGCTTTGAA 60
QY 24 ValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAla 43
DB 61 GTTAAAGTGGATGAGTGGGCTCTGGGCTGGGACATTGTGTTGTAACCTGTGC 120
QY 44 IleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAla 63
DB 121 ATCTCGAGGAAACACATTATGGATCTTTGTATCGAATGTGAGGCCAACAGGCGTCAGCT 180
QY 64 ThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisCys 83
DB 181 ACTTCGAAGAGTGTACGGTTGATGGGAGTCTGCAACCATGCTTTTCATTTCCACTGC 240
QY 84 IleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPhe 103
DB 241 ATCTCTCGATGGTCAAAACGAGCGAGGTGTGTCCTGTGGACAAACAGAGTGGGAGTTC 300
QY 104 GlnLysTyrGlyHis 108
DB 301 CAGAAGTATGGGCAT 315

RESULT 15

ABX39512

ID ABX39512 standard; cDNA; 380 BP.

XX AC ABX39512;

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

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XX AC

US2002137139-A1.

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

PT DNA Sequences encoding 7-transmembrane G-protein coupled protein
PT receptors characteristic of hematopoietic stem cells, useful for treating
PT leukemia.
XX

PS Claim 1; Page 63; 176pp; English.

XX The present invention relates to murine coding sequences for 7-
CC transmembrane G-protein coupled protein receptors (7TM-GPCRs). The
CC present sequence is one such murine 7TM-GPCR coding sequence. The present
CC sequence was derived from hematopoietic stem cells. The present sequence
CC and its corresponding protein are useful in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate 7TM-GPCR expression.
CC 7TM-GPCRs identify specific signalling molecules, to activate an effector
CC -signalling cascade that triggers an intracellular response and
CC eventually a biological effect
XX

SQ Sequence 586 BP; 140 A; 122 C; 164 G; 159 T; 0 U; 1 Other;

Alignment Scores:

Pred. No.: 1.89e-64 Length: 586
Score: 603.00 Matches: 105
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 97.89% Indels: 0
DB: 5 Gaps: 0

US-09-541-462B-2 (1-108) x AAH97862 (1-586)

QY 4 AlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArgPheGlu 23
DB 1 GCATGGATGTGGATACCCCGCGGCACCAACAGCGCGCGGCAAGAGCGCTTTGAA 60
QY 24 ValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAla 43
DB 61 GTTAAAGTGGATGAGTGGGCTCTGGGCTGGGACATTGTGTTGTAACCTGTGC 120
QY 44 IleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAla 63
DB 121 ATCTCGAGGAAACACATTATGGATCTTTGTATCGAATGTGAGGCCAACAGGCGTCAGCT 180
QY 64 ThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisCys 83
DB 181 ACTTCGAAGAGTGTACGGTTGATGGGAGTCTGCAACCATGCTTTTCATTTCCACTGC 240
QY 84 IleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPhe 103
DB 241 ATCTCTCGATGGTCAAAACGAGCGAGGTGTGTCCTGTGGACAAACAGAGTGGGAGTTC 300
QY 104 GlnLysTyrGlyHis 108
DB 301 CAGAAGTATGGGCAT 315

RESULT 15

ABX39512

ID ABX39512 standard; cDNA; 380 BP.

XX AC ABX39512;

XX AC

XX AC

XX AC

XX AC

XX AC

XX 12-JAN-1999; 99US-0115707P.
PR 11-JAN-2000; 2000US-00480902.
XX
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
PI MPI; 2003-110599/10.
XX
XX New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.
XX
XX Claim 2; SEQ ID NO 4677; 245pp; English.
XX
XX The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMPD), derived from
CC cattle, and the LMPD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMPD nucleic
CC acid linked to a promoter and a 3' non-translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and (b)
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMPD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMPD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX
SQ Sequence 380 BP; 98 A; 87 C; 103 G; 92 T; 0 U; 0 Other;

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Score: 596.00 Matches: 103
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 98.10% Mismatches: 0
Query Match: 96.75% Indels: 0
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US-09-541-462B-2 (1-108) x ABX39512 (1-380)

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Qy 24 ValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsnCysAla 43
Db 64 GTGAAAAGTGGATGACAGTACCCCTCTGGGCTGGGATATTGTGGTTGATTAACCTGTGCC 123
Qy 44 IleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAla 63
Db 124 ATCTGCAGGAACCAACATTATGATCTTTGCATAGAAATGTCAAGCCAAACAGGCGTCCGCT 183
Qy 64 ThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisCys 83
Db 184 ACTTCTGAAGAGTGCAACCGTGGCGGTCTGTGAACCATGCTTTTTCACCTTCCACTGC 243

Qy 84 IleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPhe 103
Db 244 ATCTCTCGCTGGCTCAAAACACACAGCAGGTGTCTCCGTTGGACAAACAGAGAGTGGGAATTC 303
Qy 104 GlnLysTrpGlyHis 108
Db 304 CAAAGGTATGGGCAC 318

Search completed: June 24, 2005, 09:01:45
Job time : 449 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 24, 2005, 09:58:09 ; Search time 487 Seconds
(without alignment)
1386.152 Million cell updates/sec

Title: US-09-541-462B-2
Perfect score: 616
Sequence: 1 NAAAMDVTPGTSNGAGKK.....KTRQVCPLDNREWFQKXGH 108

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6067389 seqs, 3125258755 residues

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	616	100.0	433	18	US-10-085-783A-43377	Sequence 43377, A
3	616	100.0	453	17	US-10-242-535A-35025	Sequence 35025, A
4	616	100.0	453	18	US-10-085-783A-35025	Sequence 35025, A
5	616	100.0	467	17	US-10-242-535A-39933	Sequence 39933, A
6	616	100.0	467	18	US-10-085-783A-39933	Sequence 39933, A
7	616	100.0	471	17	US-10-242-535A-57254	Sequence 57254, A
8	616	100.0	471	18	US-10-085-783A-57254	Sequence 57254, A
9	616	100.0	472	17	US-10-242-535A-56068	Sequence 56068, A
10	616	100.0	472	18	US-10-085-783A-56068	Sequence 56068, A
11	616	100.0	504	21	US-10-913-917-5	Sequence 5, Appli
12	616	100.0	508	21	US-10-913-917-3	Sequence 3, Appli
13	616	100.0	523	17	US-10-242-535A-46292	Sequence 46292, A
14	616	100.0	523	18	US-10-085-783A-46292	Sequence 46292, A
15	611	99.2	476	10	US-09-918-995-17191	Sequence 17191, A
16	607	98.5	4543	14	US-10-198-846-11311	Sequence 11311, A
17	603	97.9	430	17	US-10-242-535A-54751	Sequence 54751, A
18	603	97.9	430	18	US-10-085-783A-54751	Sequence 54751, A
19	596	96.8	380	9	US-09-960-352-4677	Sequence 4677, Ap
20	586	95.1	4476	20	US-10-357-930-25604	Sequence 25604, A
21	573	93.0	5347	16	US-10-240-965-99	Sequence 99, Appl
22	554	89.9	3484	20	US-10-723-860-1383	Sequence 1383, Ap
23	554	89.9	5111	15	US-10-205-823-382	Sequence 382, App
24	554	89.9	5371	20	US-10-723-860-5852	Sequence 5852, Ap
25	545	88.5	468	17	US-10-242-535A-47656	Sequence 47656, A
26	545	88.5	468	18	US-10-085-783A-47656	Sequence 47656, A
27	524	85.1	840	19	US-10-767-701-12172	Sequence 12172, A
28	523.5	85.0	527	21	US-10-487-901-4266	Sequence 4266, Ap
29	523.5	85.0	531	21	US-10-487-901-4271	Sequence 4271, Ap
30	523.5	85.0	586	21	US-10-487-901-4270	Sequence 4270, Ap
31	523.5	85.0	617	21	US-10-487-901-4265	Sequence 4265, Ap
32	523.5	85.0	691	21	US-10-487-901-4263	Sequence 4263, Ap
33	523.5	85.0	1259	19	US-10-437-963-11395	Sequence 11395, A
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35	521	84.6	683	21	US-10-487-901-4261	Sequence 4261, Ap
36	520	84.4	673	21	US-10-487-901-4262	Sequence 4262, Ap
37	519.5	84.3	553	19	US-10-021-323-10545	Sequence 10545, A
38	519.5	84.3	608	19	US-10-767-795-687	Sequence 687, App
39	518.5	84.2	824	18	US-10-424-599-6074	Sequence 6074, Ap
40	515.5	83.7	390	9	US-09-770-791-20	Sequence 20, Appl
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44	512	83.1	711	19	US-10-767-701-12171	Sequence 12171, A
45	509.5	82.7	486	17	US-10-242-535A-52747	Sequence 52747, A

ALIGNMENTS

RESULT 1
US-10-242-535A-43377
; Sequence 43377, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017

Db 84 CGCTTTGAAGTGAAGAGTGGATTCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 143
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 144 AACTGTGGCATCTGCAGGAACACATATTAGATCTTTGCATAGATGTCAAGCTAAACGAG 203
Qy 61 AlaSerAlaThrSerGluCysThrValAlaTTPGlyValCysAsnHisAlaPheHis 80
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Qy 81 PheHisCysIleSerArgTTPLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 264 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCATTGGACACAGAGAG 323
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Db 324 TGGGAATTCCTCAAAAGTATGGGCAC 347

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US-10-085-783A-35025
; Sequence 35025, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35025
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-35025

Alignment Scores:
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Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Qy 21 ArgPheGluValLysLysThrAsnAlaValAlaLeuTTPAlaTTPAspIleValValAsp 40
Db 84 CGCTTTGAAGTGAAGAGTGGATTCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 143
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 144 AACTGTGGCATCTGCAGGAACACATATTAGATCTTTGCATAGATGTCAAGCTAAACGAG 203
Qy 61 AlaSerAlaThrSerGluCysThrValAlaTTPGlyValCysAsnHisAlaPheHis 80
Db 204 GCGTCGGTACTTTCAGAGAGGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 263
Qy 81 PheHisCysIleSerArgTTPLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 264 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCATTGGACACAGAGAG 323

Qy 101 TrpGluPheGlnLysTyrGlyHis 108
Db 324 TGGGAATTCCTCAAAAGTATGGGCAC 347
RESULT 5
US-10-242-535A-39933
; Sequence 39933, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39933
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-39933

Alignment Scores:
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Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Db 80 CGCTTTGAAGTGAAGAGTGGATTCAGTAGCCCTCTGGGCTGGGATATTGTGGTTGAT 139
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db 140 AACTGTGGCATCTGCAGGAACACATATTAGATCTTTGCATAGATGTCAAGCTAAACGAG 199
Qy 61 AlaSerAlaThrSerGluCysThrValAlaTTPGlyValCysAsnHisAlaPheHis 80
Db 200 GCGTCGGTACTTTCAGAGAGGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 259
Qy 81 PheHisCysIleSerArgTTPLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
Db 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACAGCAGGTGTGTCATTGGACACAGAGAG 319
Qy 101 TrpGluPheGlnLysTyrGlyHis 108
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US-10-085-783A-39933
; Sequence 39933, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.

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; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
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US-10-085-783A-39933

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Score: 616.00 Matches: 108
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-09-541-462B-2 (1-108) x US-10-085-783A-39933 (1-467)

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QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuGluCysGlnAlaAsnGln 60
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QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
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QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
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QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 320 TGGGAATTCCTCAAAAGTATGGGCAC 343

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; Sequence 57254, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US 10/085,783
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57254
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-57254

Alignment Scores:
Pred. No.: 1-89e-74 Length: 471
Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-57254 (1-471)

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QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
DB 77 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 136
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuGluCysGlnAlaAsnGln 60
DB 137 AACTGTGCCATCTGCAGGAGACCAATATGGATCTTTGCATAGATGTCAGCTAACCCAG 196
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 197 GCGTCGCGTACTTCAGAGAGTGTACTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 256
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 257 TTCCTGTCATCTCTCGCTGGCTCAAAACACGACGAGGTGTCTCCATTGGACACAGAGAG 316
QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 317 TGGGAATTCCTCAAAAGTATGGGCAC 340

RESULT 8
US-10-085-783A-57254
; Sequence 57254, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US 10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57254
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-57254

Alignment Scores:
Pred. No.: 1-89e-74 Length: 471
Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0
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; SEQ ID NO 57254
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-57254

Alignment Scores:
Pred. No.: 1-89e-74 Length: 471
Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-57254 (1-471)

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DB 17 ATGGCGGAGCGATGGATGGATACCCGAGCGGCCACCAACAGCGCGCGGCAAGAG 76
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
DB 77 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 136
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuGluCysGlnAlaAsnGln 60
DB 137 AACTGTGCCATCTGCAGGAGACCAATATGGATCTTTGCATAGATGTCAGCTAACCCAG 196
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 197 GCGTCGCGTACTTCAGAGAGTGTACTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 256
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 257 TTCCTGTCATCTCTCGCTGGCTCAAAACACGACGAGGTGTCTCCATTGGACACAGAGAG 316
QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 317 TGGGAATTCCTCAAAAGTATGGGCAC 340

RESULT 8
US-10-085-783A-57254
; Sequence 57254, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US 10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57254
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-57254

Alignment Scores:
Pred. No.: 1-89e-74 Length: 471
Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0
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US-09-541-462B-2 (1-108) x US-10-085-783A-57254 (1-471)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
DB 17 ATGGCGGCGAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGCAAGAG 76
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
DB 77 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 136
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuValLysLysLysLysLysLysLys 60
DB 137 AACTGTGCACTTCAGAGAGAGTGTACTGTGCAATGATGATGATGATGATGATGATGATGAT 196
QY 61 AlaSerAlaThrSerGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 197 GCGTCCGCTACTTCAGAGAGAGTGTACTGTGCAATGATGATGATGATGATGATGATGATGAT 256
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 257 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGAG 316
QY 101 TrpGluPheGlnLysTrpGlyHis 108
DB 317 TGGGAATTCCTCAAAAGTATGGGCAC 340

RESULT 9

US-10-242-535A-56068
; Sequence 56068, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56068
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; FEATURE:
; LOCATION: (437)..(437)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (455)..(455)
; OTHER INFORMATION: n is a, c, g, or t

US-10-242-535A-56068
Alignment Scores:
Pred. No.: 1.89e-74 Length: 472
Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-56068 (1-472)
QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
DB 17 ATGGCGGCGAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGCAAGAG 76

DB 20 ATGGCGGCGAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGCAAGAG 79
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
DB 80 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 139
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuValLysLysLysLysLysLysLys 60
DB 140 AACTGTGCACTTCAGAGAGAGTGTACTGTGCAATGATGATGATGATGATGATGATGATGAT 199
QY 61 AlaSerAlaThrSerGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 200 CGTCCGCTACTTCAGAGAGAGTGTACTGTGCAATGATGATGATGATGATGATGATGATGAT 259
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACAGAGAG 319
QY 101 TrpGluPheGlnLysTrpGlyHis 108
DB 320 TGGGAATTCCTCAAAAGTATGGGCAC 343

RESULT 10

US-10-085-783A-56068
; Sequence 56068, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56068
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc feature
; FEATURE:
; LOCATION: (437)..(437)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (455)..(455)
; OTHER INFORMATION: n is a, c, g, or t

US-10-085-783A-56068
Alignment Scores:
Pred. No.: 1.89e-74 Length: 472
Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-56068 (1-472)
QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
DB 20 ATGGCGGCGAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGCGCAAGAG 79
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
DB 80 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 139

QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysGlnAlaAsnGln 60
DB 140 AACTGTGCCATCTGCAGGACCAACATTATGGATCTTTGCATAGATGTCAAGCTAACAG 199
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 200 GCCTCGCTACTTTCAGAAAGTGTACTGTGGTGGGAGTCTGTAAACCATGCTTTTTCAC 259
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 260 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGCTCCATTGGACAAACAGAG 319
QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 320 TGGGATTCAGAAAGTATGGCAT 343

RESULT 11

US-10-913-937-5
; Sequence 5, Application US/10913937
; Publication No. US20050019813A1
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklamoma Medical Research Foundation
; TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/10/913,937
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: US/09/914,324
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(344)
; OTHER INFORMATION: Rbx1
US-10-913-937-5

Alignment Scores:
Pred. No.: 2,07e-74 Length: 504
Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-913-937-5 (1-504)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
DB 18 ATGGCGCGCGCATGGATGTGGATACCCCGAGCGGACCAACAGCGCGCGGCAAG 77
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAlaAsp 40
DB 78 CGCTTTGAAGTTAAAGTGAATGCAATGAGTGGCCCTCTGGGCCCTGGGACATTTGGTTGAT 137
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysGlnAlaAsnGln 60
DB 138 AACTGTGCCATCTGCAGGACCAACATTATGGATCTTTGTATCGAATGTCAAGGCCAACAG 197
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 198 GCCTGAGCTACTTCCGAAAGTGTACGGTTGATGGGAGTCTGCAACCATGCTTTTCAT 257

QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 258 TTCCACTGCATCTCTCGATGGCTCAAAACGAGCGAGGTGTGTCGTTGGACAAACAGAG 317
QY 101 TrpGluPheGlnLysTyrGlyHis 108
DB 318 TGGGAGTTCCAGAAAGTATGGCAT 341

RESULT 12

US-10-913-937-3
; Sequence 3, Application US/10913937
; Publication No. US20050019813A1
; GENERAL INFORMATION:
; APPLICANT: Conaway, Joan A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklamoma Medical Research Foundation
; TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US/10/913,937
; CURRENT FILING DATE: 2004-08-05
; PRIOR APPLICATION NUMBER: US/09/914,324
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/121,787
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 508
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(333)
; OTHER INFORMATION: Rbx1
US-10-913-937-3

Alignment Scores:
Pred. No.: 2,09e-74 Length: 508
Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-913-937-3 (1-508)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
DB 7 ATGGCGCGCGCATGGATGTGGATACCCCGAGCGGACCAACAGCGCGCGGCAAG 66
QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAlaAsp 40
DB 67 CGCTTTGAAGTTAAAGTGAATGCAATGAGTGGCCCTCTGGGCCCTGGGATTTGGTTGAT 126
QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysGlnAlaAsnGln 60
DB 127 AACTGTGCCATCTGCAGGACCAACATTATGGATCTTTTGCATAGATGTCAAGCTAACAG 186
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 187 GCCTCGCTACTTTCAGAAAGTGTACTGTGCGCATGGGAGTCTGTAAACCATGCTTTTCAC 246
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 247 TTCCACTGCATCTCTCGCTGGCTCAAAACACGACGAGTGTGCTCCATTGGACAAACAGAG 306
QY 101 TrpGluPheGlnLysTyrGlyHis 108

Db 307 TGGGAATTCCTCAAGATGGGCAC 330

RESULT 13

US-10-242-535A-46292

; Sequence 46292, Application US/10242535A

; Publication No. US20040013663A1

; GENERAL INFORMATION:

; APPLICANT: ChondroGene Inc.

; APPLICANT: Liw, C.C.

; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

; FILE REFERENCE: 4231/2005

; CURRENT APPLICATION NUMBER: US/10/242,535A

; CURRENT FILING DATE: 2002-09-12

; PRIOR APPLICATION NUMBER: US 10/085,783

; PRIOR FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 60/305,340

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/275,017

; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: US 60/271,955

; PRIOR FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 58994

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 46292

; LENGTH: 523

; TYPE: DNA

; ORGANISM: Human

US-10-242-535A-46292

Alignment Scores:

Pred. No.:	2,18e-74	Length:	523
Score:	616.00	Matches:	108
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	17	Gaps:	0

US-09-541-462B-2 (1-108) x US-10-242-535A-46292 (1-523)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyValaGlyLysLys 20

Db 19 ATGGCGGAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGGCAAGAG 78

Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValVala 40

Db 79 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 138

Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60

Db 139 AACTGTGCATCTCGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 198

Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80

Db 199 GCGTCGCGTACTTCAGAGAGTGTACTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 258

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100

Db 259 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGGAGTGTGTCCATTGGACACAGAGAG 318

Qy 101 TrpGluPheGlnLysTrpGlyHis 108

Db 319 TGGGAATTCCTCAAGATGGGCAC 342

RESULT 14

US-10-085-783A-46292

; Sequence 46292, Application US/10085783A

; Publication No. US20040037841A1

; GENERAL INFORMATION:

; APPLICANT: ChondroGene Inc.

; APPLICANT: Liw, C.C.

; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

; FILE REFERENCE: 4231/2002

; CURRENT APPLICATION NUMBER: US/10/085,783A

; CURRENT FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 60/305,340

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/275,017

; PRIOR FILING DATE: 2001-03-12

; PRIOR APPLICATION NUMBER: US 60/271,955

; PRIOR FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 58994

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 46292

; LENGTH: 523

; TYPE: DNA

; ORGANISM: Human

US-10-085-783A-46292

Alignment Scores:

Pred. No.:	2,18e-74	Length:	523
Score:	616.00	Matches:	108
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	18	Gaps:	0

US-09-541-462B-2 (1-108) x US-10-085-783A-46292 (1-523)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20

Db 19 ATGGCGGAGCGATGGATGGATACCCCGAGCGGCACCAACAGCGCGGCAAGAG 78

Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValVala 40

Db 79 CGCTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 138

Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60

Db 139 AACTGTGCATCTCGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 198

Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80

Db 199 GCGTCGCGTACTTCAGAGAGTGTACTGCGATGGGAGTCTGTAAACCATGCTTTTCAC 258

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100

Db 259 TTCCACTGCATCTCTCGCTGGCTCAAAACACACAGGAGTGTGTCCATTGGACACAGAGAG 318

Qy 101 TrpGluPheGlnLysTrpGlyHis 108

Db 319 TGGGAATTCCTCAAGATGGGCAC 342

RESULT 15

US-09-918-995-17191

; Sequence 17191, Application US/09918995

; Publication No. US20030073623A1

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/918,995

; CURRENT FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: US/09/235,076

; PRIOR FILING DATE: 1999-01-20

; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 17191

; LENGTH: 476

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)-(476)

; OTHER INFORMATION: n = A,T,C or G

US-09-918-995-17191

Alignment Scores: 9.28e-74 Length: 476
Pred. No.: 611.00 Matches: 107
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 99.19% Indels: 0
Query Match: 10 Gaps: 0
DB: 10

US-09-541-462B-2 (1-108) x US-09-918-995-17191 (1-476)

QY	2	AlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysArg	21
DB	75	GCAGCAGCGATGGATGTGGATACCCGAGCGGCACCAACAGCGCGCGGSCAAGAGCGC	134
QY	22	PheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAspAsn	41
DB	135	TTTGAAGTCAAAAAGTGAATGCAGTAGCCCTCTGGGCCCTGGGATATTGTGGTTGATAAC	194
QY	42	CysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla	61
DB	195	TGTGCCATCTGCAGGAACCACTATTGGATCTTTGCATAGATGTCAAGCTAACCGAGCG	254
QY	62	SerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHisPhe	81
DB	255	TCGCTACTTCAGAGAGTGTACTGTGCGCATGGGAGTCTGTAACCATGCTTTTCACTTC	314
QY	82	HisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrp	101
DB	315	CACATGCATCTCTCGCTGGCTCAAAACACGACAGGTGTGTCCATTGGACACACAGAGTGG	374
QY	102	GluPheGlnLysTyrGlyHis	108
DB	375	GAATTCAAAAGTATGGGCAC	395

Search completed: June 24, 2005, 13:11:56
Job time : 489 secs

GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 24, 2005, 07:45:14 ; Search time 7486 Seconds
(without alignments)
549.151 Million cell updates/sec

Title: US-09-541-462B-2
Perfect score: 616
Sequence: 1 MAAMDVDPGTSNKGAGK.....KTRQVCPLDNREWFQKVGH 108

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blotsum62 -TRANS=human40.cdi -LIST=45
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-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09541462@cgn 1 1 3437 @runat_23062005_122624_9491 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_ges1:*
9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	616	100.0	354	5	BY344429
2	616	100.0	358	2	BB871840
3	616	100.0	358	5	BY035215
4	616	100.0	360	5	BY045296
5	616	100.0	362	5	BY099338
6	616	100.0	362	5	BY136952
7	616	100.0	362	5	BY343565
8	616	100.0	364	5	BY036231
9	616	100.0	364	5	BY090529

10	616	100.0	364	5	BY101264
11	616	100.0	370	5	BY294825
12	616	100.0	371	5	BY320216
13	616	100.0	373	5	BY065587
14	616	100.0	374	5	BY294855
15	616	100.0	375	5	BY037694
16	616	100.0	375	5	BY304291
17	616	100.0	377	5	BY041215
18	616	100.0	380	5	BY091882
19	616	100.0	381	5	BY307337
20	616	100.0	383	5	BY062504
21	616	100.0	387	5	BY291952
22	616	100.0	397	2	BE849383
23	616	100.0	401	5	BY075709
24	616	100.0	405	4	BF956282
25	616	100.0	420	5	BY263438
26	616	100.0	424	2	BF682266
27	616	100.0	432	5	BY281504
28	616	100.0	436	5	BY271641
29	616	100.0	438	6	CD287433
30	616	100.0	445	2	BF231130
31	616	100.0	448	5	BY252236
32	616	100.0	454	5	BY241321
33	616	100.0	456	2	AW461667
34	616	100.0	458	5	BY254635
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37	616	100.0	471	4	BG339057
38	616	100.0	473	5	BX283972
39	616	100.0	477	2	BF457442
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42	616	100.0	497	7	CK393930
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ALIGNMENTS

RESULT 1	BY344429	RIKEN full-length enriched, whole joints Mus musculus cDNA	354 bp	mRNA	linear	EST 12-DEC-2002
LOCUS	BY344429	clone L730004M21 5', mRNA sequence.				
DEFINITION	BY344429					
ACCESSION	BY344429					
VERSION	BY344429.1	GI:26573917				
KEYWORDS	EST.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Mus musculus					
REFERENCE	1 (bases 1 to 354)					
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Niki, K., Oshino, K., Saito, R., Suzuki, H., Yamana, K., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, N., Gojobori, T., Baldarelli, R., Hill, D. P., Bull, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Bruscia, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Kono, A. A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltas, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sadelin, A., Schneider, C., Semple, C. A., Setou, M., Shmada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wanhestedt, C., Wang, Y., Watanabe, T., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,					

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES

Location/Qualifiers

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/organism="Mus musculus"

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/db_xref="taxon:10090"

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/tissue types="whole joints"

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ORIGIN

Alignment Scores:

Fred. No.: 8.92e-61 Length: 354

Score: 616.00 Matches: 108

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 5 Gaps: 0

US-09-541-462B-2 (1-108) x BY344429 (1-354)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20

Db 15 ATGGCGCGCGGATGGATGGATGGATACCCCGCGGACCAACAGCGCGGCAAG 74

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Qy 101 TrpGluPheGlnLysTyrGlyHis 108

Db 315 TGGGAGTTCGAGAGTATGGGCAT 338

RESULT 2

BB871840 358 bp mRNA linear EST 27-NOV-2001

BB871840 RIKEN full-length enriched, 13 days embryo spinal cord Mus

musculus cDNA clone G630032107 5', mRNA sequence.

BB871840

BB871840.1 GI:17118050

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tonaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al. 2001)

REFERENCE

Unpublished (2001)

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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

JOURNAL

COMMENT

FEATURES

Location/Qualifiers

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source
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/mol_type="mRNA"
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/clone_libs="RIKEN full-length enriched, 13 days embryo
spinal cord"

ORIGIN
Alignment Scores:
Pred. No.: 9,06e-61 Length: 358
Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-541-462B-2 (1-108) x BB871840 (1-358)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyValaGlybyslys 20
Db 11 ATGGCGGGCGGCGATGGATGGATACCCCGGCGGCACACAGCGGGCGGCGAGAG 70

Qy 21 ArgPheGluValLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 40
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Qy 41 AsnCysAlaLysCysArgAsnHisLysMetAspLeuCysLysLysLysLysLysLys 60
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Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaLysLysLysLysLysLysLysLys 80
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Qy 101 TrpGluPheGlnLysTrpGlyHis 108
Db 311 TGGGAGTTCAGAGAGTATGGGCAT 334

RESULT 3
LOCUS BY035215 358 bp mRNA linear EST 06-DEC-2002
DEFINITION BY035215 RIKEN full-length enriched, 11 days pregnant adult female
placenta Mus musculus cDNA clone I530017M08 5', mRNA sequence.
ACCESSION BY035215
VERSION BY035215.1 GI:26140658
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 358)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Oeato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
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Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
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Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
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Petrovsky, N., Pillai, R., Pontius, J.U., Oi, D., Ramachandran, S.,
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Sandelin, A., Schneider, C., Semp, C.A., Setou, M., Shmida, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
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Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
12466851
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Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
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encyclopedia: real-time sequence clustering for construction of a
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cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
FEATURES
source
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ORIGIN
Alignment Scores:
Pred. No.: 9,06e-61 Length: 358
Score: 616.00 Matches: 108
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-541-462B-2 (1-108) x BY035215 (1-358)

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ACCESSION	BY045296		
VERSION	BY045296.1	GI:26150739	
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; 1 (bases 1 to 360)		
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierzki, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Akawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature	420, 563-573	(2002)
MEDLINE	22354683		
PUBMED	12468851		
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute		

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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES

source

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/organism="Mus musculus"
/mol_type="mRNA"
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ORIGIN

Alignment Scores:
Pred. No.: 9,12e-61 Length: 360
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-541-462B-2 (1-108) x BY045296 (1-360)

QY 1 MetAlaAalaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
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RESULT 5

BY099338

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY099338 362 bp mRNA linear EST 07-DEC-2002
 BY099338 RIKEN full-length enriched, pooled tissues, adult spleen,
 etc. Mus musculus cDNA clone K630127B15 5', mRNA sequence.

BY099338.1 GI:26209955

Mus musculus (house mouse)

EST.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 362)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Oato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schönbach, C., Gojōbōri, T., Baldarelli, R., Hill, D. P., Bult, C.,

Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,

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Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,

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Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, K.,

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Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,

Rogers, J., Birney, E., and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

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Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/

Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,

Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,

Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,

Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,

Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and

Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

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Normalization and subtraction of cap-trapper-selected cDNAs to

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genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

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Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

non-redundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

FEATURES

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/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="K630127B15"

/cdate="20010715"

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adult spleen, etc."

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(dev_stage=adult,tissue_type=testis,sex=male),

(dev_stage=adult,tissue_type=thymus,sex=male),

(dev_stage=adult,tissue_type=heart,sex=male),

(dev_stage=adult,tissue_type=colon,sex=male),

(dev_stage=adult,tissue_type=stomach,sex=male),

(dev_stage=adult,tissue_type=liver,sex=male),

(dev_stage=adult,tissue_type=whole

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neonate,tissue_type=brain,sex=mix),(dev_stage=10 days

neonate,tissue_type=thymus,sex=mix),(dev_stage=10 days

neonate,tissue_type=heart,sex=mix)"

ORIGIN

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Score: 9,19e-61 Length: 362

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Best Local Similarity: 100.00% Conservative: 0

Query Match: 100.00% Mismatches: 0

DB: 5 Indels: 0

Gaps: 0

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QY 21 ArgPheGluValLysLysThrAsnAlaValAlaLeuTTPAlaTTPAspIleValValAsp 40

DB 80 CGCTTTGAAGTTAAAGTGAATGAGTGGCCCTCTGGCCCTGGGACATTTGGTTGAT 139

QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60

DB 140 AACTGTGCCATCTGCAGGACACACATTTGATCTTTGATCTGATGTCAGGCCAACCCAG 199

QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTTPGlyValCysAsnHisAlaPheHis 80

DB 200 CGCTCAGCTACTTCGAAAGAGGTACGGTTGATCGATGGGAGTCTGCAACCATCTTTTCAT 259

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DB 260 TTCACACTGCATCTCTCGATGGCTCAAAACAGGCGAGGTGTGTCCGTGGACACAGAGAG 319

QY 101 TrpGluPheGlnLysTyrGlyHis 108

DB 320 TGGGAGTTCCAGAGTATGGGCAT 343

RESULT 6

BY136952

LOCUS

DEFINITION

ACCESSION

VERSION

BY136952

BY136952 RIKEN full-length enriched, 17.5 days embryo whole body

Mus musculus cDNA clone L930084016 5', mRNA sequence.

BY136952

BY136952.1 GI:26272503

362 bp mRNA linear EST 09-DEC-2002

KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 362)	
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaído, I., Osato, R., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierzki, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Perlea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reid, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sanderlin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Komno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.	
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	
JOURNAL	Nature 420, 563-573 (2002)	
MEDLINE	22354683	
PUBMED	12466851	
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Tel: 81-45-503-9216 Fax: 81-45-503-9216 Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/ Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. please visit our web site (http://genome.gsc.riken.go.jp) for further details. Location/Qualifiers 1. .362 /organism="Mus musculus"	
FEATURES		
source		

ORIGIN		
Alignment Scores:		
Prod. No.:	9.19e-61	Length: 362
Score:	616.00	Matches: 108
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
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DB:	5	Gaps: 0
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Db	23 ATGGCGCGCGCGCATGGATGGATACCCCGCGGCCCAACAGCGCGCGGCAAGAG 82	
QY	21 ArGpHeGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40	
Db	83 CGCTTTGAAGTTAAAGATGGAATGCAGTGGCCCTCTGGGCTGGGACATTGTGTTGAT 142	
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LOCUS	362 bp mRNA linear EST 12-DEC-2002	
DEFINITION	BY343565 RIKEN full-length enriched, whole joints Mus musculus cDNA clone L230046F06 5', mRNA sequence.	
ACCESSION	BY343565	
VERSION	BY343565.1 GI:26573053	
KEYWORDS	EST.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 362)	
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaído, I., Osato, R., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierzki, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Perlea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reid, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sanderlin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Komno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.	

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 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.
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ORIGIN

Alignment Scores:
 Pred. No.: 9,266-61 Length: 364
 Score: 616.00 Matches: 108
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0

US-09-541-462B-2 (1-108) x BY036231 (1-364)

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 Qy 21 ArgPheGluValLysLysTpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
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 Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
 Db 262 TTCCACTGCATCTCTCGATGGCTCAAAACGAGGAGGTGTGTCTGCTTGGACACAGAGAG 321
 Qy 101 TrpGluPheGlnLysTyrGlyHis 108
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Db 322 TGGGAGTTCCAGAGTATGGCAT 345

RESULT 9
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 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
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 ORGANISM
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 AUTHORS

BY090529 364 bp mRNA linear EST 07-DEC-2002
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 BY090529
 BY090529.1 GI:26199768
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 364)
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
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 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
 Versardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L.G., Wynnshaw-Boris, A., Yanagisawa, M., Yang, I.,
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Inotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 22354683
 12466851
 Contact: Yoshihide Hayashizaki
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 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Inotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
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 cDNA library was prepared and sequenced in Mouse Genome

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Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES

source

Location/Qualifiers

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Alignment Scores:

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Pred. No.: 9,266-61 Length: 364
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Percent Similarity: 100.00% Conservative: 0
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US-09-541-462B-2 (1-108) x BY090529 (1-364)

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DB 323 TGGGAGTTCACAGAGTATGGGCAT 346
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RESULT 10

BY101264

LOCUS

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BY101264 RIKEN full-length enriched, 15 days pregnant adult female
amion Mus musculus cDNA clone K630136007 5', mRNA sequence.
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ACCESSION

BY101264

VERSION

EST.

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 364)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

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FEATURES

source

Location/Qualifiers

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/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="K630136007"
/sex="female"
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/clone_lib="RIKEN full-length enriched, 15 days pregnant
adult female amion"
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ORIGIN

Alignment Scores:

Pred. No.:

9,266-61

Length:

364

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reid, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sanderlin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

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2354683

12466851

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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

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 DB: 5 Gaps: 0

US-09-541-462B-2 (1-108) x BY101264 (1-364)

QY 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
 Db 15 ATGGCGCGCGGATGGATGGATACCCCGAGCGGACCAACAGCGCGCGGCAAGAAG 74
 QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
 Db 75 CGCTTTGAAGTTAAAAGTGGATGCAGTGGCCCTCTGGGCTGGGACATTGGTTGAT 134
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 Db 135 AACTGTGCCATCTGCAGGACCAACATATTATGATCTTTGATCATGATGTCAGGCGCAACAG 194
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RESULT 11

LOCUS BY294825 370 bp mRNA linear EST 11-DEC-2002
 DEFINITION BY294825 RIKEN full-length enriched, visual cortex Mus musculus
 cDNA clone K530330G11 5', mRNA sequence.

ACCESSION BY294825

VERSION BY294825.1 GI:26485162

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 370)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

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Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

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JOURNAL MEDLINE
 PUBLISHED COMMENT

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prepare mouse tissues.

Tissues were provided by Michela Pagiolini and Takao K. Hensch (

Laboratory for Neuronal Circuit Development Brain Science Institute

RIKEN 2-1 Hirotsawa, Wako-shi, Saitama 351-0198 Japan) whose

assistance we gratefully acknowledge. Please visit our web site

(http://genome.gsc.riken.go.jp) for further details.

Location/Qualifiers

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Pred. No.: 9,466-61 Length: 370

Score: 616.00 Matches: 108

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Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 5 Gaps: 0

US-09-541-462B-2 (1-108) x BY294825 (1-370)

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Db 30 ATGGCGCGCGGATGGATGGATACCCCGAGCGGACCAACAGCGCGCGGCAAGAAG 89

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Db 90 CGCTTTGAAGTTAAAAGTGGATGCAGTGGCCCTCTGGGCTGGGACATTGGTTGAT 149

QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60

Db 150 AACTGTGCCATCTGCAGGACCAACATATTATGATCTTTGATCGAATGTAGGCCCAACAG 209

QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80

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QY      101 TrpGluPheGlnYsTrpGlyHis 108
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RESULT 12
BY320216
LOCUS   BY320216 RIKEN full-length enriched, osteoclast-like cell Mus
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE  Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS

1 (bases 1 to 371)
Oikazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
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Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
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Division of Experimental Animal Research in Riken contributed to
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Tissues were provided by Takashi Ishikawa ( Department of Surgery
2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama
236-0004 Japan ) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
FEATURES             Location/Qualifiers
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                     /clone="I420104M17"
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                     /clone_libs="RIKEN full-length enriched, osteoclast-like
                     cell"
ORIGIN
Alignment Scores:
Pred. No.:          9,496-61      Length:      371
Score:              616.00      Matches:    108
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:        100.00%      Indels:      0
DB:                  5           Gaps:        0
US-09-541-462B-2 (1-108) x BY320216 (1-371)
QY      1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyValaGlyLysLys 20
Db      30 ATGGCGGGGGGATGGATGTGGATATACCCCGAGCCACCAACAGCGCGCGGCGAGAG 89
QY      21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
Db      90 CGCTTTGAAGTTAAAGTGGAAATGCAGTGGCCCTCTGGCCCTGGGACATTGTGTTGAT 149
QY      41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
Db      150 AACTGTGCCCATCTGCAGGAACCAACATTATGGATCTTTGTATCGAATGTGAGCCCAACAG 209
QY      61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
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QY      81 PheHisCysIleSerArgTrpLeuYsThrArgGlnValCysProLeuAspAenArgGlu 100
Db      270 TTCCACTGCATCTCTCGATGGCTCAAAACGAGGAGGTGTGTCGTCGACCAACAGAGAG 329
QY      101 TrpGluPheGlnYsTrpGlyHis 108
Db      330 TGGGAGTTCAGAAGTATGGGCAT 353

RESULT 13
BY065587
LOCUS   BY065587 RIKEN full-length enriched, 17 days embryo kidney Mus
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE  Mus musculus (house mouse)

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ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 373)

REFERENCE
AUTHORS

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
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Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
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Analysis of the mouse transcriptome based on functional annotation
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TITLE

JOURNAL
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COMMENT

Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>
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Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

FEATURES
source

Location/Qualifiers
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/organism="Mus musculus"
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/strain="C57BL/6J"

/db_xref="taxon:10090"
/clone="I920043D08"
/tissue_type="kidney"
/dev_stage="17 days embryo"
/clone_lib="RIKEN full-length enriched, 17 days embryo
kidney"

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Score: 616.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0
US-09-541-462b-2 (1-108) x BY065587 (1-373)
QY 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20
DB 13 ATGGCGCGCGCGATGGATCGGATACCCCGCGCGGCCACACAGCGCGCGGCAAGAAG 72
QY 21 ArgPheGluValIysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40
DB 73 CGCTTTGAAGTTAAAGTGAATGCAGTGGCCCTCTGGGCGCTGGGACATTTGTGTTGAT 132
QY 41 AsnCyeAlaIleCyeArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60
DB 133 AACTGTGGCCATCTGCAGGAACACATATTGGATCTTTGTATCGAATGTGAGGCCAACCCAG 192
QY 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80
DB 193 GCGTCAGCTACTTCGAGAGAGTGACGGTTGCATGGGAGTCTGCAACCATGCTTTTCAT 252
QY 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100
DB 253 TTCCACTGCATCTCTCGATGGCTCAAAACGAGCGAGGTGTGTCGTTGGACACAGAGAG 312
QY 101 TrpGluPheGlnLysTrpGlyHis 108
DB 313 TGGGAGGTTCCAGAAGTATGGGCAT 336

RESULT 14

BY294855 374 bp mRNA linear EST 11-DEC-2002
BY294855 RIKEN full-length enriched, visual cortex Mus musculus
CDNA clone K530330K07 5', mRNA sequence.
BY294855
BY294855.1 GI:26485192
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 374)

ACCESSION
VERSION

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KEYWORDS

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